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OM protein - protein search, using sw model

Run on: December 4, 2003, 18:07:22 ; Search time 22 Seconds
(without alignments)
51.927 Million cell updates/sec

Title: US-09-897-412-10
Perfect score: 132
Sequence: 1 HSDGFTFTSELSRLREGARLQRLLQGLV 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB ID	
<hr/>						
1	132	100.0	27	1	US-07-924-054-10	Sequence 10, Appl
2	132	100.0	27	1	US-08-062-472B-43	Sequence 43, Appl
3	123	93.2	27	1	US-08-519-180-6	Sequence 6, Appl
4	123	93.2	27	2	US-08-818-253-36	Sequence 36, Appl
5	123	93.2	27	3	US-08-818-252-36	Sequence 36, Appl
6	123	93.2	27	4	US-09-260-846-18	Sequence 18, Appl
7	123	93.2	27	4	US-08-842-322-30	Sequence 30, Appl
8	123	93.2	27	4	US-09-316-919-52	Sequence 52, Appl
9	120	90.9	27	1	US-07-822-924-10	Sequence 10, Appl
10	120	90.9	27	5	PCT-US93-00683-10	Sequence 10, Appl
11	108.5	82.2	26	1	US-07-776-272-25	Sequence 25, Appl

12	67	50.8	320	4	US-09-252-991A-30676	Sequence 30676, A
13	62	47.0	31	4	US-09-209-799D-26	Sequence 26, Appl
14	62	47.0	31	4	US-09-997-792A-23	Sequence 23, Appl
15	61	46.2	37	3	US-09-302-596-11	Sequence 11, Appl
16	61	46.2	37	4	US-09-333-415-11	Sequence 11, Appl
17	61	46.2	37	4	US-09-303-016-11	Sequence 11, Appl
18	61	46.2	37	4	US-09-805-507-11	Sequence 11, Appl
19	61	46.2	38	1	US-08-519-180-9	Sequence 9, Appli
20	61	46.2	38	3	US-09-302-596-10	Sequence 10, Appl
21	61	46.2	38	4	US-09-333-415-10	Sequence 10, Appl
22	61	46.2	38	4	US-09-303-016-10	Sequence 10, Appl
23	61	46.2	38	4	US-09-805-507-10	Sequence 10, Appl
24	60	45.5	31	4	US-09-209-799D-24	Sequence 24, Appl
25	60	45.5	31	4	US-09-997-792A-21	Sequence 21, Appl
26	60	45.5	39	1	US-08-066-480-1	Sequence 1, Appli
27	60	45.5	39	3	US-09-302-596-7	Sequence 7, Appli
28	60	45.5	39	4	US-09-623-618B-11	Sequence 11, Appl
29	60	45.5	39	4	US-09-333-415-7	Sequence 7, Appli
30	60	45.5	39	4	US-09-303-016-7	Sequence 7, Appli
31	60	45.5	39	4	US-09-323-867A-1	Sequence 1, Appli
32	60	45.5	39	4	US-09-657-332A-11	Sequence 11, Appl
33	60	45.5	39	4	US-09-805-507-7	Sequence 7, Appli
34	60	45.5	40	4	US-09-623-618B-19	Sequence 19, Appl
35	60	45.5	40	4	US-09-623-618B-33	Sequence 33, Appl
36	60	45.5	40	4	US-09-623-618B-34	Sequence 34, Appl
37	60	45.5	40	4	US-09-657-332A-19	Sequence 19, Appl
38	60	45.5	40	4	US-09-657-332A-33	Sequence 33, Appl
39	60	45.5	40	4	US-09-657-332A-34	Sequence 34, Appl
40	59	44.7	29	1	US-07-741-931-2	Sequence 2, Appli
41	59	44.7	29	1	US-08-066-480-7	Sequence 7, Appli
42	59	44.7	29	1	US-08-255-558B-1	Sequence 1, Appli
43	59	44.7	29	1	US-08-255-558B-7	Sequence 7, Appli
44	59	44.7	29	1	US-07-937-132A-2	Sequence 2, Appli
45	59	44.7	29	1	US-08-473-334B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-07-924-054-10

; Sequence 10, Application US/07924054

; Patent No. 5486472

; GENERAL INFORMATION:

; APPLICANT: SUZUKI, No. 5486472uhiro

; APPLICANT: KITADA, Chieko

; APPLICANT: TSUDA, Masao

; TITLE OF INVENTION: ANTIBODY TO PACAP AND USE THEREOF

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS&

; ADDRESSEE: CUSHMAN

; STREET: 130 Water Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: US

; ZIP: 02109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/924,054
; FILING DATE: 19920903
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 40805
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-07-924-054-10

Query Match 100.0%; Score 132; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.2e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 HSDGTFTSELSRLREGARLQRLLQGLV 27

RESULT 2

US-08-062-472B-43

; Sequence 43, Application US/08062472B
; Patent No. 5695954

; GENERAL INFORMATION:

; APPLICANT: Sherwood, Nancy G M
; APPLICANT: Parker, David B
; APPLICANT: McRory, John E
; APPLICANT: Lescheid, David W
; TITLE OF INVENTION: DNA ENCODING TWO FISH NEUROPEPTIDES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: KLARQUIST, SPARKMAN, CAMPBELL, LEIGH &
; ADDRESSEE: WHINSTON, LLP
; STREET: ONE WORLD TRADE CENTER, SUITE 1600, 121 S.W.
; STREET: SALMON STREET
; CITY: PORTLAND
; STATE: OREGON
; COUNTRY: USA
; ZIP: 97204-2988

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/062,472B
; FILING DATE: 14-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: POLLEY, RICHARD J
; REGISTRATION NUMBER: 28107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-062-472B-43

Query Match 100.0%; Score 132; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.2e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||| ||| ||| ||| ||| ||| ||| |||
Db 1 HSDGTFTSELSRLREGARLQRLLQGLV 27

RESULT 3

US-08-519-180-6

; Sequence 6, Application US/08519180

; Patent No. 5770570

; GENERAL INFORMATION:

; APPLICANT: PAUL, SUDHIR
; APPLICANT: YASUKO, NODA
; APPLICANT: ISRAEL, RUBINSTEIN
; TITLE OF INVENTION: A METHOD OF DELIVERING A VASOACTIVE
; TITLE OF INVENTION: INTESTINAL POLYPEPTIDE, AN ENCAPSULATED VASOACTIVE
; TITLE OF INVENTION: INTESTINAL POLYPEPTIDE, AND A METHOD OF MAKING THE
; TITLE OF INVENTION: ENCAPSULATED VASOACTIVE INTESTINAL POLYPEPTIDE
; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/519,180

; FILING DATE: 25-AUG-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/224488
; FILING DATE: 07-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SEMINAUER, JEFFREY A.
; REGISTRATION NUMBER: 31,933
; REFERENCE/DOCKET NUMBER: 4464/98971
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-519-180-6

Query Match 93.2%; Score 123; DB 1; Length 27;
Best Local Similarity 92.6%; Pred. No. 1.1e-11;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
| | | | | | | | | | | | : | | | | | | | |
Db 1 HSDGTFTSELSRLRDSARLQRLLQGLV 27

RESULT 4

US-08-818-253-36

; Sequence 36, Application US/08818253
; Patent No. 5998204
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,253
; FILING DATE: 14-MAR-1997
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/043001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-818-253-36

Query Match 93.2%; Score 123; DB 2; Length 27;
Best Local Similarity 92.6%; Pred. No. 1.1e-11;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|||:|||||:|||||
Db 1 HSDGTFTSELSRLRDSARLQRLLQGLV 27

RESULT 5

US-08-818-252-36

; Sequence 36, Application US/08818252B
; Patent No. 6197928
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/08/818,252B
; CURRENT FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Sus scrofa

US-08-818-252-36

Query Match 93.2%; Score 123; DB 3; Length 27;
Best Local Similarity 92.6%; Pred. No. 1.1e-11;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|||:|||||:|||||
Db 1 HSDGTFTSELSRLRDSARLQRLLQGLV 27

RESULT 6

US-09-260-846-18

; Sequence 18, Application US/09260846
; Patent No. 6307017
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Moreau, Jacques-Pierre
; APPLICANT: Kim, Sun Hyuk
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS
; FILE REFERENCE: 00537/00900J
; CURRENT APPLICATION NUMBER: US/09/260,846
; CURRENT FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 27
; TYPE: PRT
; ORGANISM: mammalian
; FEATURE:
; OTHER INFORMATION: Porcine/Bovine
; FEATURE:
; OTHER INFORMATION: this peptide has an amidated c-terminus
US-09-260-846-18

Query Match 93.2%; Score 123; DB 4; Length 27;
Best Local Similarity 92.6%; Pred. No. 1.1e-11;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
| | | | | | | | | | | | : | | | | | | | |
Db 1 HSDGTFTSELSRLRDSARLQRLLQGLV 27

RESULT 7

US-08-842-322-30

; Sequence 30, Application US/08842322
; Patent No. 6376257
; GENERAL INFORMATION:
; APPLICANT: Persechini, Anthony
; TITLE OF INVENTION: DETECTION BY FRET CHANGES OF LIGAND
; TITLE OF INVENTION: BINDING BY GFP FUSION PROTEINS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,322
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:

; NAME: BRAMAN, SUSAN J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 176/60170
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-842-322-30

Query Match 93.2%; Score 123; DB 4; Length 27;
Best Local Similarity 92.6%; Pred. No. 1.1e-11;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||| ||| | | | | : | | | | | | | |
Db 1 HSDGTFTSELSRLRDSARLQRLLQGLV 27

RESULT 8

US-09-316-919-52
; Sequence 52, Application US/09316919
; Patent No. 6469154
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Baird, Geoffrey
; TITLE OF INVENTION: FLUORESCENT PROTEIN INDICATORS
; FILE REFERENCE: 07257/073001
; CURRENT APPLICATION NUMBER: US/09/316,919
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Sus scrofa

US-09-316-919-52

Query Match 93.2%; Score 123; DB 4; Length 27;
Best Local Similarity 92.6%; Pred. No. 1.1e-11;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||| ||| | | | | : | | | | | | | |
Db 1 HSDGTFTSELSRLRDSARLQRLLQGLV 27

RESULT 9

US-07-822-924-10
; Sequence 10, Application US/07822924
; Patent No. 5258453
; GENERAL INFORMATION:

; APPLICANT: J. Kopecek et al.
; TITLE OF INVENTION: A DRUG DELIVERY SYSTEM FOR THE
; TITLE OF INVENTION: SIMULTANEOUS DELIVERY OF DRUGS ACTIVATABLE BY ENZYMES
AND
; TITLE OF INVENTION: LIGHT
; NUMBER OF SEQUENCES: Ten
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thorpe, No. 5258453th & Western
; STREET: 9035 South 700 East, Suite 200
; CITY: Sandy
; STATE: Utah
; COUNTRY: USA
; ZIP: 84070
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
; COMPUTER: compaq LTE/286
; OPERATING SYSTEM: DOS 4.01
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/822,924
; FILING DATE: 19920121
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: na
; ATTORNEY/AGENT INFORMATION:
; NAME: Western, M. Wayne
; REGISTRATION NUMBER: 22,788
; REFERENCE/DOCKET NUMBER: T377
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801) 566-6633
; TELEFAX: (801) 566-0750
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-822-924-10

Query Match 90.9%; Score 120; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 3.1e-11;
Matches 24; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
| | | | | | | | | | | | : | | | | | | | |
Db 1 HSDGTFTSELSRLRDSARLERLLQGLV 27

RESULT 10
PCT-US93-00683-10
; Sequence 10, Application PC/TUS9300683
; GENERAL INFORMATION:
; APPLICANT: J. Kopecek et al.
; TITLE OF INVENTION: A DRUG DELIVERY SYSTEM FOR THE
; TITLE OF INVENTION: SIMULTANEOUS DELIVERY OF DRUGS ACTIVATABLE BY ENZYMES
AND
; TITLE OF INVENTION: LIGHT

; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thorpe, North & Western
; STREET: 9035 South 700 East, Suite 200
; CITY: Sandy
; STATE: Utah
; COUNTRY: USA
; ZIP: 84070
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
; COMPUTER: compaq LTE/286
; OPERATING SYSTEM: DOS 4.01
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00683
; FILING DATE: 19930121
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/822,924
; FILING DATE: 21 JAN 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Western, M. Wayne
; REGISTRATION NUMBER: 22,788
; REFERENCE/DOCKET NUMBER: T377
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801) 566-6633
; TELEFAX: (801) 566-0750
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27
; TYPE: AMINO ACID
; TOPOLOGY: linear
PCT-US93-00683-10

Query Match 90.9%; Score 120; DB 5; Length 27;
Best Local Similarity 88.9%; Pred. No. 3.1e-11;
Matches 24; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
| | | | | | | | | | | | : | | | | | | | |
Db 1 HSDGTFTSELSRLRDSARLERLLQGLV 27

RESULT 11
US-07-776-272-25
; Sequence 25, Application US/07776272
; Patent No. 5612454
; GENERAL INFORMATION:
; APPLICANT: Kaminuma, Toshihiko
; APPLICANT: Iida, Toshii
; APPLICANT: Tajima, Masahiro
; TITLE OF INVENTION: Process for Purification of Polypeptide
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wegner, Cantor, Mueller & Player
; STREET: 1233 20th St. N.W. P.O. Box 18218
; CITY: Washington

; STATE: District of Columbia
; COUNTRY: United States of America
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/776,272
; FILING DATE: 19911129
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P-450-23167
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-0400
; TELEFAX: 202-887-0605
; TELEX: 440706
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES

US-07-776-272-25

Query Match 82.2%; Score 108.5; DB 1; Length 26;
Best Local Similarity 88.9%; Pred. No. 1.5e-09;
Matches 24; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
Db 1 HSDGTFTSE-SRLRDSARLQRLLQGLV 26

RESULT 12

US-09-252-991A-30676
; Sequence 30676, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30676
; LENGTH: 320

; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30676

Query Match 50.8%; Score 67; DB 4; Length 320;
Best Local Similarity 82.4%; Pred. No. 0.031;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DGTFTSELSRLREGARL 19
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Db 140 DGEFTSELSRLREGDQL 156

RESULT 13

US-09-209-799D-26

; Sequence 26, Application US/09209799D
; Patent No. 6380357
; GENERAL INFORMATION:
; APPLICANT: Hermeling, Ronald
; APPLICANT: Hoffmann, James
; APPLICANT: Narasimhan, Chakravarthy
; TITLE OF INVENTION: GLUCAGON-LIKE PEPTIDE-1 CRYSTALS
; FILE REFERENCE: X-10242
; CURRENT APPLICATION NUMBER: US/09/209,799D
; CURRENT FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-209-799D-26

Query Match 47.0%; Score 62; DB 4; Length 31;
Best Local Similarity 44.4%; Pred. No. 0.013;
Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
| : | : | : | | | : : |
Db 1 HAEGTFTSDVSSYLEGQRAKEFIawlV 27

RESULT 14

US-09-997-792A-23

; Sequence 23, Application US/09997792A
; Patent No. 6555521
; GENERAL INFORMATION:
; APPLICANT: ELI LILLY and COMPANY
; TITLE OF INVENTION: Glucagon-Like Peptide-1 Crystals
; FILE REFERENCE: X-10242A
; CURRENT APPLICATION NUMBER: US/09/997,792A
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US 60/069,728
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-997-792A-23

Query Match 47.0%; Score 62; DB 4; Length 31;
Best Local Similarity 44.4%; Pred. No. 0.013;
Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
| : | | | | : | | | | : | |
Db 1 HAEGTFTSDVSSYLEGQRAKEFIAWLV 27

RESULT 15
US-09-302-596-11
; Sequence 11, Application US/09302596
; Patent No. 6284725
; GENERAL INFORMATION:
; APPLICANT: Coolidge, Thomas R.
; APPLICANT: Ehlers, Mario R.W.
; TITLE OF INVENTION: Metabolic Intervention with GLP-1 to Improve the Function
of
; TITLE OF INVENTION: Ischemic and Reperfused Tissue
; FILE REFERENCE: P03660US1
; CURRENT APPLICATION NUMBER: US/09/302,596
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/103,498
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Gila Monster venom
US-09-302-596-11

Query Match 46.2%; Score 61; DB 3; Length 37;
Best Local Similarity 44.4%; Pred. No. 0.022;
Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
| | | | | : | | : | | | : | : ::
Db 1 HSDATFTAESKLLAKLALQKYLESIL 27

Search completed: December 4, 2003, 18:10:43
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2003, 18:09:26 ; Search time 31 Seconds
(without alignments)
161.986 Million cell updates/sec

Title: US-09-897-412-10
Perfect score: 132

Sequence: 1 HSDGTFTELSRLREGARLQRLLQGLV 27

Scoring table: BLOSUM62
Gapext 0.5 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match Length	DB ID	Description
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1	132	100.0	27	10	US-09-897-412-10	Sequence 10, Appl
2	132	100.0	27	15	US-10-197-954-123	Sequence 123, App
3	126	95.5	27	10	US-09-897-412-12	Sequence 12, Appl
4	123	93.2	27	10	US-09-897-412-11	Sequence 11, Appl
5	123	93.2	27	10	US-09-999-745-52	Sequence 52, Appl
6	123	93.2	27	10	US-09-554-000-36	Sequence 36, Appl
7	123	93.2	27	15	US-10-004-530A-19	Sequence 19, Appl
8	65	49.2	29	11	US-09-847-249A-10	Sequence 10, Appl
9	64	48.5	29	11	US-09-847-249A-30	Sequence 30, Appl
10	64	48.5	29	11	US-09-847-249A-38	Sequence 38, Appl
11	64	48.5	29	11	US-09-847-249A-73	Sequence 73, Appl
12	64	48.5	29	11	US-09-847-249A-74	Sequence 74, Appl
13	64	48.5	29	11	US-09-847-249A-75	Sequence 75, Appl
14	64	48.5	29	11	US-09-847-249A-76	Sequence 76, Appl
15	63	47.7	29	11	US-09-847-249A-25	Sequence 25, Appl
16	63	47.7	29	11	US-09-847-249A-28	Sequence 28, Appl
17	63	47.7	29	11	US-09-847-249A-34	Sequence 34, Appl
18	63	47.7	29	11	US-09-847-249A-44	Sequence 44, Appl
19	62	47.0	29	11	US-09-847-249A-9	Sequence 9, Appl
20	62	47.0	29	11	US-09-847-249A-11	Sequence 11, Appl
21	62	47.0	30	15	US-10-265-345A-4	Sequence 4, Appl
22	62	47.0	31	11	US-09-997-792-26	Sequence 26, Appl
23	61	46.2	29	11	US-09-847-249A-32	Sequence 32, Appl
24	61	46.2	29	11	US-09-847-249A-40	Sequence 40, Appl
25	61	46.2	29	11	US-09-847-249A-66	Sequence 66, Appl
26	61	46.2	29	11	US-09-847-249A-67	Sequence 67, Appl
27	61	46.2	29	11	US-09-847-249A-70	Sequence 70, Appl
28	61	46.2	37	9	US-09-851-738-11	Sequence 11, Appl
29	61	46.2	37	9	US-09-805-507-11	Sequence 11, Appl
30	61	46.2	37	10	US-09-859-804-11	Sequence 11, Appl
31	61	46.2	37	10	US-09-982-978-11	Sequence 11, Appl
32	61	46.2	37	10	US-09-953-021B-11	Sequence 11, Appl
33	61	46.2	37	15	US-10-091-258-11	Sequence 11, Appl
34	61	46.2	37	15	US-10-055-259-11	Sequence 11, Appl
35	61	46.2	37	15	US-10-197-954-81	Sequence 81, Appl
36	61	46.2	38	9	US-09-851-738-10	Sequence 10, Appl
37	61	46.2	38	9	US-09-805-507-10	Sequence 10, Appl
38	61	46.2	38	10	US-09-859-804-10	Sequence 10, Appl
39	61	46.2	38	10	US-09-982-978-10	Sequence 10, Appl
40	61	46.2	38	10	US-09-953-021B-10	Sequence 10, Appl
41	61	46.2	38	15	US-10-091-258-10	Sequence 10, Appl
42	61	46.2	38	15	US-10-055-259-10	Sequence 10, Appl
43	61	46.2	38	15	US-10-197-954-80	Sequence 80, Appl
44	60	45.5	31	11	US-09-997-792-24	Sequence 24, Appl
45	60	45.5	39	9	US-09-876-388-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-09-897-412-10

; Sequence 10, Application US/09897412

; Patent No. US20020142956A1

; GENERAL INFORMATION:

; APPLICANT: Davis, Richard J

; APPLICANT: Page, Keith J
; TITLE OF INVENTION: Use of Secretin-Receptor Ligands in Treatment of Cystic
; TITLE OF INVENTION: Fibrosis (CF) and Chronic Obstructive Pulmonary Disease
; TITLE OF INVENTION: (COPD)
; FILE REFERENCE: 620-148
; CURRENT APPLICATION NUMBER: US/09/897,412
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: GB 0016441.8
; PRIOR FILING DATE: 2000-07-04
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-412-10

Query Match 100.0%; Score 132; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
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Db 1 HSDGTFTSELSRLREGARLQRLLQGLV 27

RESULT 2
US-10-197-954-123
; Sequence 123, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K"ster, Hubert
; APPLICANT: Siddiqi, Suhaib
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 123
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-197-954-123

Query Match 100.0%; Score 132; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
 ||||| ||||| ||||| |||||
Db 1 HSDGTFTSELSRLREGARLQRLLQGLV 27

RESULT 3

US-09-897-412-12

; Sequence 12, Application US/09897412
; Patent No. US20020142956A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Richard J
; APPLICANT: Page, Keith J
; TITLE OF INVENTION: Use of Secretin-Receptor Ligands in Treatment of Cystic
; TITLE OF INVENTION: Fibrosis (CF) and Chronic Obstructive Pulmonary Disease
; TITLE OF INVENTION: (COPD)
; FILE REFERENCE: 620-148
; CURRENT APPLICATION NUMBER: US/09/897,412
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: GB 0016441.8
; PRIOR FILING DATE: 2000-07-04
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Canis sp.

US-09-897-412-12

Query Match 95.5%; Score 126; DB 10; Length 27;
Best Local Similarity 96.3%; Pred. No. 4.1e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
 ||||| ||||| ||||| |||||
Db 1 HSDGTFTSELSRLRESARLQRLLQGLV 27

RESULT 4

US-09-897-412-11

; Sequence 11, Application US/09897412
; Patent No. US20020142956A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Richard J
; APPLICANT: Page, Keith J
; TITLE OF INVENTION: Use of Secretin-Receptor Ligands in Treatment of Cystic
; TITLE OF INVENTION: Fibrosis (CF) and Chronic Obstructive Pulmonary Disease
; TITLE OF INVENTION: (COPD)
; FILE REFERENCE: 620-148
; CURRENT APPLICATION NUMBER: US/09/897,412
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: GB 0016441.8
; PRIOR FILING DATE: 2000-07-04
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 27

; TYPE: PRT
; ORGANISM: Sus sp.
US-09-897-412-11

Query Match 93.2%; Score 123; DB 10; Length 27;
Best Local Similarity 92.6%; Pred. No. 1.2e-11;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
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Db 1 HSDGTFTSELSRLRDSARLQRLLQGLV 27

RESULT 5

US-09-999-745-52
; Sequence 52, Application US/09999745
; Patent No. US20020157120A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Baird, Geoffrey
; TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
; FILE REFERENCE: REGEN1470-1
; CURRENT APPLICATION NUMBER: US/09/999,745
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 09/316,920
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 52
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-999-745-52

Query Match 93.2%; Score 123; DB 10; Length 27;
Best Local Similarity 92.6%; Pred. No. 1.2e-11;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||| ||| ||| : ||| ||| |||
Db 1 HSDGTFTSELSRLRDSARLQRLLQGLV 27

RESULT 6

US-09-554-000-36
; Sequence 36, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/09/554,000
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 08/818,252

; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-554-000-36

Query Match 93.2%; Score 123; DB 10; Length 27;
Best Local Similarity 92.6%; Pred. No. 1.2e-11;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||| ||| | | | | : | | | | | | | |
Db 1 HSDGTFTSELSRLRDSARLQRLLQGLV 27

RESULT 7

US-10-004-530A-19
; Sequence 19, Application US/10004530A
; Publication No. US20030050436A1
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Moreau, Jacques-Pierre
; APPLICANT: Kim, Sun H.
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS
; FILE REFERENCE: 00537-00900K
; CURRENT APPLICATION NUMBER: US/10/004,530A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/260,846
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 08/337,127
; PRIOR FILING DATE: 1994-11-10
; PRIOR APPLICATION NUMBER: 07/779,039
; PRIOR FILING DATE: 1991-10-18
; PRIOR APPLICATION NUMBER: 07/502,438
; PRIOR FILING DATE: 1990-03-30
; PRIOR APPLICATION NUMBER: 07/397,169
; PRIOR FILING DATE: 1989-08-21
; PRIOR APPLICATION NUMBER: 07/376,555
; PRIOR FILING DATE: 1989-07-07
; PRIOR APPLICATION NUMBER: 07/317,941
; PRIOR FILING DATE: 1989-03-02
; PRIOR APPLICATION NUMBER: 07/282,328
; PRIOR FILING DATE: 1988-12-09
; PRIOR APPLICATION NUMBER: 07/257,998
; PRIOR FILING DATE: 1988-10-14
; PRIOR APPLICATION NUMBER: 07/248,771
; PRIOR FILING DATE: 1988-09-23
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-004-530A-19

Query Match 93.2%; Score 123; DB 15; Length 27;
Best Local Similarity 92.6%; Pred. No. 1.2e-11;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
| | | | | | | | : | | | | | | |
Db 1 HSDGTFTSELSRLRDSARLQRLLQGLV 27

RESULT 8

US-09-847-249A-10

; Sequence 10, Application US/09847249A
; Publication No. US20030032588A1
; GENERAL INFORMATION:
; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: STARK, KEVIN LEE
; TITLE OF INVENTION: GLUCAGON ANTAGONIST
; FILE REFERENCE: A-693
; CURRENT APPLICATION NUMBER: US/09/847,249A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,436
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Glucagon Antagonist

US-09-847-249A-10

Query Match 49.2%; Score 65; DB 11; Length 29;
Best Local Similarity 51.9%; Pred. No. 0.007;
Matches 14; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
| | | | | | | | : | | | | | | |
Db 1 HSQGTFTSEYSRYLDSRRAQDFVQWLM 27

RESULT 9

US-09-847-249A-30

; Sequence 30, Application US/09847249A
; Publication No. US20030032588A1
; GENERAL INFORMATION:
; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: STARK, KEVIN LEE
; TITLE OF INVENTION: GLUCAGON ANTAGONIST
; FILE REFERENCE: A-693
; CURRENT APPLICATION NUMBER: US/09/847,249A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,436
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 80

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Glucagon Antagonist
US-09-847-249A-30

Query Match 48.5%; Score 64; DB 11; Length 29;
Best Local Similarity 48.1%; Pred. No. 0.0099;
Matches 13; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|| ||||| |: : | | :| |:
Db 1 HSQGTFTSEYSKYLDSRRAQEFVQWLM 27

RESULT 10
US-09-847-249A-38
; Sequence 38, Application US/09847249A
; Publication No. US20030032588A1
; GENERAL INFORMATION:
; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: STARK, KEVIN LEE
; TITLE OF INVENTION: GLUCAGON ANTAGONIST
; FILE REFERENCE: A-693
; CURRENT APPLICATION NUMBER: US/09/847,249A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,436
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Glucagon Antagonist
US-09-847-249A-38

Query Match 48.5%; Score 64; DB 11; Length 29;
Best Local Similarity 48.1%; Pred. No. 0.0099;
Matches 13; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|| ||||| |: : | | :| |:
Db 1 HSQGTFTSEYSKYLDSRRAQEFVQWLM 27

RESULT 11
US-09-847-249A-73
; Sequence 73, Application US/09847249A
; Publication No. US20030032588A1
; GENERAL INFORMATION:
; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: STARK, KEVIN LEE

; TITLE OF INVENTION: GLUCAGON ANTAGONIST
; FILE REFERENCE: A-693
; CURRENT APPLICATION NUMBER: US/09/847,249A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,436
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiment
; NAME/KEY: misc_feature
; LOCATION: (29)..(29)
; OTHER INFORMATION: Fc domain at the C-terminus attached through an optional linker

US-09-847-249A-73

Query Match 48.5%; Score 64; DB 11; Length 29;
Best Local Similarity 48.1%; Pred. No. 0.0099;
Matches 13; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
 || | | | | | | : : | | : | | :
Db 1 HSQGTFTSEYSKYLDSSRRAQEFVQWLM 27

RESULT 12

US-09-847-249A-74

; Sequence 74, Application US/09847249A
; Publication No. US20030032588A1
; GENERAL INFORMATION:
; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: STARK, KEVIN LEE
; TITLE OF INVENTION: GLUCAGON ANTAGONIST
; FILE REFERENCE: A-693
; CURRENT APPLICATION NUMBER: US/09/847,249A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,436
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiment
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Fc domain at the N-terminus attached through an optional linker

US-09-847-249A-74

Query Match 48.5%; Score 64; DB 11; Length 29;

Best Local Similarity 48.1%; Pred. No. 0.0099;
Matches 13; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|| ||||| | : : | | : | |:
Db 1 HSQGTFTSEYSKYLDSRRAQEFVQWLM 27

RESULT 13

US-09-847-249A-75

; Sequence 75, Application US/09847249A
; Publication No. US20030032588A1
; GENERAL INFORMATION:
; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: STARK, KEVIN LEE
; TITLE OF INVENTION: GLUCAGON ANTAGONIST
; FILE REFERENCE: A-693
; CURRENT APPLICATION NUMBER: US/09/847,249A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,436
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiment
; NAME/KEY: misc_feature
; LOCATION: (29)..(29)
; OTHER INFORMATION: Fc domain at the C-terminus attached through an optional linker

US-09-847-249A-75

Query Match 48.5%; Score 64; DB 11; Length 29;
Best Local Similarity 48.1%; Pred. No. 0.0099;
Matches 13; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|| ||||| | : : | | : | |:
Db 1 HSQGTFTSEYSKYLDSRRAQEFVQWLM 27

RESULT 14

US-09-847-249A-76

; Sequence 76, Application US/09847249A
; Publication No. US20030032588A1
; GENERAL INFORMATION:
; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: STARK, KEVIN LEE
; TITLE OF INVENTION: GLUCAGON ANTAGONIST
; FILE REFERENCE: A-693
; CURRENT APPLICATION NUMBER: US/09/847,249A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,436
; PRIOR FILING DATE: 2000-05-03

; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiment
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Fc domain at the N-terminus attached through an optional linker
US-09-847-249A-76

Query Match 48.5%; Score 64; DB 11; Length 29;
Best Local Similarity 48.1%; Pred. No. 0.0099;
Matches 13; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|| ||||| | : : | | : | | :
Db 1 HSQGTFTSEYSKYLDSRRAQEFVQWLM 27

RESULT 15

US-09-847-249A-25

; Sequence 25, Application US/09847249A
; Publication No. US20030032588A1
; GENERAL INFORMATION:
; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: STARK, KEVIN LEE
; TITLE OF INVENTION: GLUCAGON ANTAGONIST
; FILE REFERENCE: A-693
; CURRENT APPLICATION NUMBER: US/09/847,249A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,436
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Glucagon Antagonist
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: Xaa is norleucine (Nle)
US-09-847-249A-25

Query Match 47.7%; Score 63; DB 11; Length 29;
Best Local Similarity 48.1%; Pred. No. 0.014;
Matches 13; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|| ||||| | : : | | : | | :
Db 1 HSQGTFTSEYSKYLDSRRAQXFVQWLM 27

Search completed: December 4, 2003, 18:15:05
Job time : 32 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2003, 18:07:22 ; Search time 35 Seconds
(without alignments)
199.069 Million cell updates/sec

Title: US-09-897-412-10
Perfect score: 132
Sequence: 1 HSDGTFTSELSRLREGARLQRLLQGLV 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:
1: sp_archea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rat:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	%		
No.	Score	Match Length	DB ID	Description

1	67	50.8	258	16	Q9HVH6	
2	59	44.7	176	6	Q8MJ25	Q9hv6 pseudomonas
3	59	44.7	180	6	Q95LG0	Q8mj25 ovis aries
4	59	44.7	220	13	Q8UWL9	Q95lg0 canis famil
5	56	42.4	170	6	Q8MI77	Q8uw19 hoplobatrac
6	56	42.4	171	11	Q9D2Z7	Q8mi77 bos taurus
7	55	41.7	121	13	Q9DDE6	Q9d2z7 mus musculu
8	52	39.4	178	13	Q91971	Q9dde6 brachydanio
9	52	39.4	421	13	Q9PUD5	Q91971 oncorhynchus
10	51	38.6	38	5	Q8IU39	Q9pud5 xenopus lae
11	51	38.6	38	5	Q8IU38	Q8iu39 dugesia jap
12	51	38.6	38	5	Q8IU37	Q8iu38 hydra magni
13	51	38.6	38	5	Q8IU36	Q8iu37 sepioteuthi
14	51	38.6	38	13	Q8AYP5	Q8iu36 periplaneta
15	51	38.6	38	13	Q8AYP4	Q8ayp5 trachurus j
16	51	38.6	138	13	Q98SP4	Q8ayp4 acipenser s
17	51	38.6	170	11	Q8BJT8	Q98sp4 oncorhynchus
18	51	38.6	171	13	Q9PUF8	Q8bjt8 mus musculu
19	51	38.6	172	13	Q9DE29	Q9puf8 xenopus lae
20	51	38.6	173	13	Q98SP5	Q9de29 brachydanio
21	51	38.6	175	13	Q90XZ4	Q98sp5 oncorhynchus
22	50.5	38.3	275	16	Q8FDI6	Q90xz4 ictalurus p
23	50	37.9	560	13	Q9PUD4	Q8fdi6 escherichia
24	49	37.1	479	11	Q9QWV7	Q9pud4 xenopus lae
25	49	37.1	545	16	Q92W00	Q9qwv7 mus musculu
26	48	36.4	175	13	Q98TU3	Q92w00 rhizobium m
27	48	36.4	207	17	Q9HKE7	Q98tu3 brachydanio
28	48	36.4	292	11	Q8C9T0	Q9hke7 thermoplasm
29	48	36.4	450	4	Q8N681	Q8c9t0 mus musculu
30	48	36.4	495	10	Q8S2J6	Q8n681 homo sapien
31	48	36.4	505	11	Q9CWN7	Q8s2j6 oryza sativ
32	48	36.4	510	4	Q9UKZ1	Q9cwn7 mus musculu
33	48	36.4	1169	17	Q9YAT8	Q9ukz1 homo sapien
34	47.5	36.0	293	16	Q9A7P0	Q9yat8 aeropyrum p
35	47.5	36.0	835	5	Q8SWB2	Q9a7p0 caulobacter
36	47	35.6	28	13	Q9PRI9	Q8swb2 encephalito
37	47	35.6	387	16	Q97S18	Q9pri9 amia calva
38	47	35.6	425	2	Q9S4J2	Q97s18 streptococc
39	47	35.6	425	16	Q8DQS4	Q9s4j2 streptococc
40	47	35.6	441	10	Q8L846	Q8dqs4 streptococc
41	47	35.6	698	2	Q9Z486	Q8l846 arabidopsis
42	47	35.6	1409	13	Q8JI27	Q9z486 aeromonas p
43	47	35.6	1428	13	Q8AY67	Q8ji27 brachydanio
44	47	35.6	2089	10	Q39478	Q8ay67 brachydanio
45	46.5	35.2	137	17	Q979T5	Q39478 cyclotella
						Q979t5 thermoplasm

ALIGNMENTS

RESULT 1

Q9HVH6

ID Q9HVH6 PRELIMINARY; PRT; 258 AA.
AC Q9HVH6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Probable oxidoreductase.
GN PA4615.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RL Nature 406:959-964 (2000).
DR EMBL; AE004875; AAG08003.1; -.
DR HSSP; P28861; 1FDR.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR InterPro; IPR001221; Phe_hydroxylase.
DR Pfam; PF00970; FAD_binding_6; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR PRINTS; PR00371; FPNCR.
DR PRINTS; PR00410; PHEHYDRXLASE.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29377 MW; 2EB12D1A2CF92E5F CRC64;

Query Match 50.8%; Score 67; DB 16; Length 258;
Best Local Similarity 82.4%; Pred. No. 0.058;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DGTFTSELSRLREGARL 19
|| ||||| : |
Db 78 DGEFTSELSRLREGDQL 94

RESULT 2
Q8MJ25
ID Q8MJ25 PRELIMINARY; PRT; 176 AA.
AC Q8MJ25;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Preproglucagon (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;

RA Limesand S.W., Hay W.W. Jr.;
 RT "Characterization of the endocrine pancreas in an ovine placental
 insufficiency IUGR fetus.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF529185; AAM94409.1; -.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 3.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 3.
 DR PROSITE; PS00260; GLUCAGON; 2.
 FT NON_TER 176 176
 SQ SEQUENCE 176 AA; 20335 MW; 13174039BD6CE2B3 CRC64;

 Query Match 44.7%; Score 59; DB 6; Length 176;
 Best Local Similarity 44.4%; Pred. No. 0.61;
 Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

 Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
 || |||||: |: : | | :| |:
 Db 53 HSQGTFTSDYSKYLDSRRAQDFVQWLM 79

RESULT 3
 Q95LG0
 ID Q95LG0 PRELIMINARY; PRT; 180 AA.
 AC Q95LG0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Preproglucagon.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Irwin D.M.;
 RT "cDNA cloning of proglucagon from the stomach and pancreas of the
 RT dog.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF308439; AAL09425.1; -.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 3.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 3.
 DR PROSITE; PS00260; GLUCAGON; 2.
 SQ SEQUENCE 180 AA; 21114 MW; 80F66941AFC324FD CRC64;

 Query Match 44.7%; Score 59; DB 6; Length 180;
 Best Local Similarity 44.4%; Pred. No. 0.63;
 Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

 Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
 || |||||: |: : | | :| |:
 Db 53 HSQGTFTSDYSKYLDSRRAQDFVQWLM 79

RESULT 4

Q8UWL9

ID Q8UWL9 PRELIMINARY; PRT; 220 AA.

AC Q8UWL9;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Proglucagon.

OS Hoplobatrachus rugulosus.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;

OC Hoplobatrachus.

OX NCBI_TaxID=110072;

RN [1]

RP SEQUENCE FROM N.A.

RA Yeung C.-M., Chow B.K.C.;

RT "Identification of a proglucagon cDNA from *Rana tigrina rugulosa* that encodes two GLP-1s.";

RL Gen. Comp. Endocrinol. 124:0-0 (2001).

DR EMBL; AF324209; AAL35758.1; -.

DR InterPro; IPR000532; Glucagon.

DR Pfam; PF00123; hormone2; 4.

DR PRINTS; PR00275; GLUCAGON.

DR SMART; SM00070; GLUCA; 4.

DR PROSITE; PS00260; GLUCAGON; 4.

SQ SEQUENCE 220 AA; 25615 MW; C72D926E7F89E381 CRC64;

Query Match 44.7%; Score 59; DB 13; Length 220;
Best Local Similarity 44.4%; Pred. No. 0.79;
Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|| | ||| : | : : | | : | |:
Db 53 HSQGTFTSDYSKYLDSRRAQDFVQWLM 79

RESULT 5

Q8MI77

ID Q8MI77 PRELIMINARY; PRT; 170 AA.

AC Q8MI77;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Vasoactive intestinal polypeptide precursor.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22092342; PubMed=12097482;

RA Hamelink C., Lee H.-W., Chen Y., Grimaldi M., Eiden L.E.;

RT "Coincident elevation of cAMP and calcium influx by PACAP-27 synergistically regulates vasoactive intestinal polypeptide gene transcription through a novel PKA-independent signaling pathway.";

RL J. Neurosci. 22:5310-5320 (2002).

DR EMBL; AF503910; AAM28152.1; -.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 2.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 2.
 DR PROSITE; PS00260; GLUCAGON; 2.
 KW Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 81 107 PHI.
 FT CHAIN 125 152 VIP.
 SQ SEQUENCE 170 AA; 19164 MW; 9C6A6049AF7BFF81 CRC64;

 Query Match 42.4%; Score 56; DB 6; Length 170;
 Best Local Similarity 40.7%; Pred. No. 1.7;
 Matches 11; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

 Qy 1 HSDGTFTSELSRLREGARLQRLQQGLV 27
 | : || | ||: ||| :: | : |:
 Db 81 HADGVFTSDYSRLLGQLSAKKYLESLI 107

RESULT 6
 Q9D2Z7
 ID Q9D2Z7 PRELIMINARY; PRT; 171 AA.
 AC Q9D2Z7;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Vasoactive intestinal polypeptide.
 GN VIP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."

RL Nature 409:685-690 (2001).
DR EMBL; AK018599; BAB31301.1; -.
DR MGD; MGI:98933; Vip.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 2.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 2.
DR PROSITE; PS00260; GLUCAGON; 2.
SQ SEQUENCE 171 AA; 19135 MW; 134A434DB6DF1254 CRC64;

Query Match 42.4%; Score 56; DB 11; Length 171;
Best Local Similarity 40.7%; Pred. No. 1.7;
Matches 11; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|:||| |||: ||| :; |: |:
Db 82 HADGVFTSDYSRLLGQISAKKYLESLI 108

RESULT 7
Q9DDE6
ID Q9DDE6 PRELIMINARY; PRT; 121 AA.
AC Q9DDE6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Glucagon polyprotein.
GN GCG OR GLU.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99425190; PubMed=10495291;
RA Argenton F., Zecchin E., Bortolussi M.;
RT "Early appearance of pancreatic hormone-expressing cells in the
RT zebrafish embryo.";
RL Mech. Dev. 87:217-221(1999).
DR EMBL; AJ133697; CAC20108.1; -.
DR HSSP; P01274; 1GCN.
DR ZFIN; ZDB-GENE-010219-1; gcg.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 2.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 2.
DR PROSITE; PS00260; GLUCAGON; 2.
KW Polyprotein.
FT CHAIN 49 79 GLUCAGON.
FT CHAIN 88 121 GLUCAGON-LIKE PEPTIDE 1.
SQ SEQUENCE 121 AA; 13537 MW; A85385F690DA180F CRC64;

Query Match 41.7%; Score 55; DB 13; Length 121;
Best Local Similarity 40.7%; Pred. No. 1.6;
Matches 11; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HSDGFTSELSRLREGARLQRLLQGLV 27
||:||||::|:|_|_|_|_|_|:
Db 50 HSEGTFNSNDYSKYLETRRAQDFVQWLM 76

RESULT 8

Q91971

ID Q91971 PRELIMINARY; PRT; 178 AA.
AC Q91971; Q91408; Q91188; Q92169;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Glucagon I precursor.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=DISTAL SMALL INTESTINE, AND PANCREAS;
RX MEDLINE=95295739; PubMed=7776976;
RA Irwin D.M., Wong J.;
RT "Trout and chicken proglucagon: alternative splicing generates mRNA
transcripts encoding glucagon-like peptide 2.";
RL Mol. Endocrinol. 9:267-277(1995).
CC -!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
CC THE BLOOD SUGAR LEVEL (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; INTESTINAL (SHOWN HERE) AND
CC PANCREATIC; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN
CC RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR EMBL; U19913; AAC59667.1; -.
DR EMBL; U19917; AAC59669.1; -.
DR EMBL; U19918; AAC60212.1; -.
DR EMBL; U19919; AAC60213.1; -.
DR EMBL; U19918; AAC60213.1; JOINED.
DR EMBL; S78475; AAB34505.1; -.
DR EMBL; S78473; AAB34504.2; -.
DR HSSP; P01274; 1GCN.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 3.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 3.
DR PROSITE; PS00260; GLUCAGON; 3.
KW Glucagon family; Hormone; Cleavage on pair of basic residues; Signal;
KW Alternative splicing; Multigene family.
FT SIGNAL 1 ? POTENTIAL.
FT PEPTIDE ? 49 GRPP (GLICENTINE RELATED POLYPEPTIDE).
FT PEPTIDE 52 80 GLUCAGON.
FT PEPTIDE 85 120 GLUCAGON-LIKE PEPTIDE 1.
FT PEPTIDE 137 169 GLUCAGON-LIKE PEPTIDE 2.
FT VARSPlic 124 178 MISSING (IN PANCREATIC ISOFORM).
SQ SEQUENCE 178 AA; 20034 MW; 5CF6980CF2A9D58E CRC64;

Query Match 39.4%; Score 52; DB 13; Length 178;

Best Local Similarity 37.0%; Pred. No. 7.2;
Matches 10; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||:||||::|:| :| | :| |:
Db 52 HSEGTFNSNDYSKYQEERMAQDFVQWLM 78

RESULT 9

Q9PUD5

ID Q9PUD5 PRELIMINARY; PRT; 421 AA.
AC Q9PUD5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Synapsin I (Fragment).
GN SYN I.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kao H.-T., Porton B., Hilfiker S., Stefani G., Pieribone V.A.,
RA DeSalle R., Greengard P.;
RT "Molecular Evolution of the Synapsin Gene Family.";
RL J. Exp. Zool. 0:0-0(2000).
DR EMBL; AF192751; AAF08809.1; -.
DR HSSP; P17599; 1AUX.
DR InterPro; IPR001359; Synapsin.
DR Pfam; PF02078; Synapsin; 1.
DR Pfam; PF02750; Synapsin_C; 1.
DR PRINTS; PR01368; SYNAPSIN.
DR PROSITE; PS00415; SYNAPSIN_1; 1.
DR PROSITE; PS00416; SYNAPSIN_2; 1.
FT NON_TER 421 421
SQ SEQUENCE 421 AA; 46067 MW; EC73182AD569BCFF CRC64;

Query Match 39.4%; Score 52; DB 13; Length 421;
Best Local Similarity 41.7%; Pred. No. 19;
Matches 10; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
Qy 1 HSDGTFTSELSRLREGARLQRLLQ 24
||:||:||: :| ||| | ::| | :|:
Db 137 HSNGSFSDLEVLRNGVKVVRSLK 160

RESULT 10

Q8IU39

ID Q8IU39 PRELIMINARY; PRT; 38 AA.
AC Q8IU39;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pituitary adenylate cyclase activating polypeptide (Fragment).
GN ADCYAP1.

OS Dugesia japonica (Planarian).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesiidae; Dugesia.
OX NCBI_TaxID=6161;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoshino M., Ogata M., Ikeya K., Watanabe K.;
RT "Pituitary Adenylate Cyclase Activating Polypeptide (PACAP),
RT Planarian.";
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB083649; BAC21155.1; -.
FT NON_TER 1 1
FT NON_TER 38 38
SQ SEQUENCE 38 AA; 4655 MW; BFD29C49770AF065 CRC64;

Query Match 38.6%; Score 51; DB 5; Length 38;
Best Local Similarity 37.0%; Pred. No. 1.8;
Matches 10; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
| | | | | | | : : : | : :
Db 1 HSDGIFTDSYSRYRKQMAVKKYLAABL 27

RESULT 11

Q8IU38
ID Q8IU38 PRELIMINARY; PRT; 38 AA.
AC Q8IU38;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pituitary adenylate cyclase activating polypeptide (Fragment).
GN ADCYAP1.
OS Hydra magnipapillata (Hydra).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6085;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoshino M., Ogata M., Ikeya K., Fujisawa T.;
RT "Pituitary Adenylate Cyclase Activating Polypeptide (PACAP), Hydra.";
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB083650; BAC21156.1; -.
FT NON_TER 1 1
FT NON_TER 38 38
SQ SEQUENCE 38 AA; 4655 MW; BFD29C49770AF065 CRC64;

Query Match 38.6%; Score 51; DB 5; Length 38;
Best Local Similarity 37.0%; Pred. No. 1.8;
Matches 10; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
| | | | | | | : : : | : :
Db 1 HSDGIFTDSYSRYRKQMAVKKYLAABL 27

RESULT 12

Q8IU37

ID Q8IU37 PRELIMINARY; PRT; 38 AA.

AC Q8IU37;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Pituitary adenylate cyclase activating polypeptide (Fragment).

GN ADCYAP1.

OS Sepioteuthis lessoniana.

OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoeloidea;

OC Decapodiformes; Loliginidae; Sepioteuthis.

OX NCBI_TaxID=34570;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Hoshino M., Ogata M., Ikeya K., Mihara S.;

RT "Pituitary Adenylate Cyclase Activating Polypeptide (PACAP), Big fin reef squid.";

RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AB083651; BAC21157.1; -.

FT NON_TER 1 1

FT NON_TER 38 38

SQ SEQUENCE 38 AA; 4655 MW; BFD29C49770AF065 CRC64;

Query Match 38.6%; Score 51; DB 5; Length 38;
Best Local Similarity 37.0%; Pred. No. 1.8;
Matches 10; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||| || | : :: | ::
Db 1 HSDGIFTDSYSRYRKQMAVKKYLAABL 27

RESULT 13

Q8IU36

ID Q8IU36 PRELIMINARY; PRT; 38 AA.

AC Q8IU36;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Pituitary adenylate cyclase activating polypeptide (Fragment).

GN ADCYAP1.

OS Periplaneta americana (American cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;

OC Blattidae; Periplaneta.

OX NCBI_TaxID=6978;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Hoshino M., Ogata M., Ikeya K., Mihara S.;

RT "Pituitary Adenylate Cyclase Activating Polypeptide (PACAP), American cockroach.";

RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AB083652; BAC21158.1; -.

FT NON_TER 1 1

FT NON_TER 38 38

SQ SEQUENCE 38 AA; 4628 MW; BFC36C49770AF065 CRC64;
Query Match 38.6%; Score 51; DB 5; Length 38;
Best Local Similarity 37.0%; Pred. No. 1.8;
Matches 10; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
Qy 1 HSDGIFTSELSRLREGARLQRLLQGLV 27
||| || | : :: | ::
Db 1 HSDGIFTDSYSRYRKQMAVKKYLAABL 27

RESULT 14

Q8AYP5
ID Q8AYP5 PRELIMINARY; PRT; 38 AA.
AC Q8AYP5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pituitary adenylate cyclase activating polypeptide (Fragment).
GN ADCYAP1.
OS Trachurus japonicus (Japanese jack mackerel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC Carangidae; Trachurus.
OX NCBI_TaxID=83875;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Hoshino M., Ogata M., Ikeya K., Mihara S.;
RT "Pituitary Adenylate Cyclase Activating Polypeptide (PACAP), Japanese
RT horse mackerel.";
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB083647; BAC21153.1; -.
FT NON_TER 1 1
FT NON_TER 38 38
SQ SEQUENCE 38 AA; 4605 MW; BFD29C52770AF065 CRC64;

Query Match 38.6%; Score 51; DB 13; Length 38;
Best Local Similarity 37.0%; Pred. No. 1.8;
Matches 10; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
Qy 1 HSDGIFTSELSRLREGARLQRLLQGLV 27
||| || | : :: | ::
Db 1 HSDGIFTDSYSRYRKQMAVKKYLAABL 27

RESULT 15

Q8AYP4
ID Q8AYP4 PRELIMINARY; PRT; 38 AA.
AC Q8AYP4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pituitary adenylate cyclase activating polypeptide (Fragment).
GN ADCYAP1.
OS Acipenser schrenckii (Amur sturgeon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;
OC Acipenser.
OX NCBI_TaxID=111304;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Hoshino M., Ogata M., Ikeya K., Mihara S.;
RT "Pituitary Adenylate Cyclase Activating Polypeptide (PACAP), Amur
RT sturgeon.";
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB083648; BAC21154.1; -.
FT NON_TER 1 1
FT NON_TER 38 38
SQ SEQUENCE 38 AA; 4591 MW; BFD29C40E70AF065 CRC64;

Query Match 38.6%; Score 51; DB 13; Length 38;
Best Local Similarity 37.0%; Pred. No. 1.8;
Matches 10; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
| | | | | | | : :: | ::
Db 1 HSDGIFTDSYSRYRKQMAVKKYLAABL 27

Search completed: December 4, 2003, 18:10:11
Job time : 39 secs

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OM protein - protein search, using sw model

Run on: December 4, 2003, 18:07:22 ; Search time 11 Seconds
(without alignments)
115.429 Million cell updates/sec

Title: US-09-897-412-10
Perfect score: 132
Sequence: 1 HSDGTFTSELSRLREGARLQRLLQGLV 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query Score	Match	Length	DB	ID	Description
1	132	100.0	121	1	SECR_HUMAN	P09683 homo sapien
2	126	95.5	27	1	SECR_CANFA	P09910 canis famil
3	123	93.2	27	1	SECR_SHEEP	P31299 ovis aries
4	123	93.2	131	1	SECR_PIG	P01279 sus scrofa
5	119	90.2	134	1	SECR_RAT	P11384 rattus norv
6	113	85.6	133	1	SECR_MOUSE	Q08535 mus musculu
7	112	84.8	27	1	SECR_RABIT	P32647 oryctolagus
8	78	59.1	27	1	SECR_CHICK	P01280 gallus gall
9	61	46.2	38	1	EXE1_HELSU	P04203 heloderma s
10	61	46.2	180	1	GLUC_CAVPO	P05110 cavia porce
11	60	45.5	39	1	EXE3_HELHO	P20394 heloderma h
12	59	44.7	29	1	GLUC_DIDMA	P18108 didelphis m
13	59	44.7	29	1	GLUC_RABIT	P25449 oryctolagus
14	59	44.7	69	1	GLUC_CANFA	P29794 canis famil
15	59	44.7	103	1	GLUC_RANCA	P15438 rana catesb
16	59	44.7	158	1	GLUC_PIG	P01274 sus scrofa
17	59	44.7	180	1	GLUC_BOVIN	P01272 bos taurus

18	59	44.7	180	1	GLUC_HUMAN	P01275 homo sapien
19	59	44.7	180	1	GLUC_MESAU	P01273 mesocricetu
20	59	44.7	180	1	GLUC_MOUSE	P55095 mus musculu
21	59	44.7	180	1	GLUC_RAT	P06883 rattus norv
22	59	44.7	204	1	GLUC_HELSU	O12956 heloderma s
23	59	44.7	206	1	GLUC_CHICK	P01277 gallus gall
24	59	44.7	219	1	GLU2_XENLA	O42144 xenopus lae
25	59	44.7	266	1	GLU1_XENLA	O42143 xenopus lae
26	58	43.9	62	1	GLUC_SCYCA	P09687 scyliorhinu
27	57	43.2	29	1	GLUC_ANAPL	P01276 anas platyr
28	57	43.2	29	1	GLUC_TORMA	P09567 torpedo mar
29	57	43.2	72	1	VIP_PIG	P01284 sus scrofa
30	57	43.2	72	1	VIP_RABIT	P32649 oryctolagus
31	56	42.4	72	1	VIP_BOVIN	P81401 bos taurus
32	56	42.4	72	1	VIP_CAVPO	P04566 cavia porce
33	56	42.4	170	1	VIP_MOUSE	P32648 mus musculu
34	56	42.4	170	1	VIP_RAT	P01283 rattus norv
35	56	42.4	180	1	GLUC_OCTDE	P22890 octodon deg
36	55	41.7	38	1	PACA_URAJA	P81039 uranoscopuss
37	55	41.7	71	1	GLUC_ICTPU	P04093 ictalurus p
38	55	41.7	71	1	GLUC_PIAME	P81880 piaractus m
39	55	41.7	75	1	GLUC_AMICA	P33528 amia calva
40	54	40.9	29	1	GLUC_PLAFE	P23062 platichthys
41	54	40.9	78	1	GLUC_LEPSP	P09566 lepisosteus
42	54	40.9	96	1	GLUC_MYOSC	P09686 myoxocephal
43	54	40.9	122	1	GLU2_LOPAM	P04092 lophius ame
44	53	40.2	29	1	GLUC_CALMI	P13189 callorhynch
45	52	39.4	29	1	GLUC_CHIBR	P31297 chinchilla

ALIGNMENTS

RESULT 1

SECR_HUMAN

ID SECR_HUMAN STANDARD; PRT; 121 AA.
 AC P09683;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Secretin precursor.
 GN SCT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20515579; PubMed=11060443;
 RA Whitmore T.E., Holloway J.L., Lofton-Day C.E., Maurer M.F., Chen L.,
 RA Quinton T.J., Vincent J.B., Scherer S.W., Lok S.;
 RT "Human secretin (SCT): gene structure, chromosome location, and
 distribution of mRNA.";
 RL Cytogenet. Cell Genet. 90:47-52(2000).
 RN [2]
 RP SEQUENCE OF 28-54.
 RA Carlquist M., Joernvall H., Forssmann W.-G., Thulin L., Johansson C.,

RA Mutt V.;
 RT "Human secretin is not identical to the porcine/bovine hormone.";
 RL IRCS Med. Sci. 13:217-218(1985).
 CC -!- FUNCTION: STIMULATES FORMATION OF NAHCO(3)-RICH PANCREATIC JUICE
 CC AND SECRETION OF NAHCO(3)-RICH BILE AND INHIBITS HCL PRODUCTION
 CC BY THE STOMACH.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF244355; AAG31443.1; -.
 DR Genew; HGNC:10607; SCT.
 DR MIM; 182099; -.
 DR GO; GO:0005180; F:peptide hormone; NAS.
 DR GO; GO:0030157; P:pancreatic juice secretion; NAS.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Hormone; Amidation;
 KW Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT PEPTIDE 28 54 SECRETIN.
 FT MOD_RES 54 54 AMIDATION (G-55 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 121 AA; 13016 MW; 44BDB4EFC0E161CF CRC64;

 Query Match 100.0%; Score 132; DB 1; Length 121;
 Best Local Similarity 100.0%; Pred. No. 7.1e-13;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 HSDGTFTSELSRLREGARLQRLQQGLV 27
 |||||||
 Db 28 HSDGTFTSELSRLREGARLQRLQQGLV 54

RESULT 2
 SECR_CANFA
 ID SECR_CANFA STANDARD PRT; 27 AA.
 AC P09910;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Secretin.
 GN SCT.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;

RX MEDLINE=87314204; PubMed=3626755;
RA Shinomura Y., Eng J., Yalow R.S.;
RT "Dog secretin: sequence and biologic activity.";
RL Life Sci. 41:1243-1248 (1987).
CC -!- FUNCTION: STIMULATES FORMATION OF NAHCO(3)-RICH PANCREATIC JUICE
CC AND SECRETION OF NAHCO(3)-RICH BILE AND INHIBITS HCL PRODUCTION
CC BY THE STOMACH.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR; A27267; A27267.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Hormone; Amidation.
FT MOD_RES 27 27 AMIDATION.
SQ SEQUENCE 27 AA; 3070 MW; 2D4015814F955B78 CRC64;

Query Match 95.5%; Score 126; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 HSDGTFTSELSRLRESARLQRLLQGLV 27

RESULT 3
SECR_SHEEP
ID SECR_SHEEP STANDARD; PRT; 27 AA.
AC P31299;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Secretin.
GN SCT.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Small intestine;
RX MEDLINE=91239834; PubMed=2034821;
RA Bounjoua Y., Vandermeers A., Robberecht P., Vandermeers-Piret M.C.,
RA Christophe J.;
RT "Purification and amino acid sequence of vasoactive intestinal
RT peptide, peptide histidine isoleucinamide and secretin from the ovine
RT small intestine.";
RL Regul. Pept. 32:169-179(1991).
CC -!- FUNCTION: STIMULATES FORMATION OF NAHCO(3)-RICH PANCREATIC JUICE
CC AND SECRETION OF NAHCO(3)-RICH BILE AND INHIBITS HCL PRODUCTION
CC BY THE STOMACH.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR; C60072; SESH.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.

DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Hormone; Amidation.
FT MOD_RES 27 27 AMIDATION.
SQ SEQUENCE 27 AA; 3056 MW; 2D4015814ED05B78 CRC64;

Query Match 93.2%; Score 123; DB 1; Length 27;
Best Local Similarity 92.6%; Pred. No. 3.1e-12;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|||:|||||:|||||
Db 1 HSDGTFTSELSRLRDSARLQRLLQGLV 27

RESULT 4
SECR_PIG
ID SECR_PIG STANDARD; PRT; 131 AA.
AC P01279; Q9TR13;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Secretin precursor (Fragment).
GN SCT.
OS Sus scrofa (Pig),
OS Bos taurus (Bovine), and
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823, 9913, 10141;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Pig;
RX MEDLINE=90192795; PubMed=2315322;
RA Kopin A.S., Wheeler M.B., Leiter A.B.;
RT "Secretin: structure of the precursor and tissue distribution of the mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:2299-2303(1990).
RN [2]
RP SEQUENCE OF 1-56.
RC SPECIES=Pig;
RC TISSUE=Intestine;
RX MEDLINE=96109189; PubMed=8618828;
RA Bonetto V., Joernvall H., Mutt V., Sillard R.;
RT "Two alternative processing pathways for a preprohormone: a bioactive form of secretin.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:11985-11989(1995).
RN [3]
RP SEQUENCE OF 30-56.
RC SPECIES=Pig;
RX MEDLINE=70282334; PubMed=5465996;
RA Mutt V., Jorpes J.E., Magnusson S.;
RT "Structure of porcine secretin. The amino acid sequence.";
RL Eur. J. Biochem. 15:513-519(1970).
RN [4]
RP SEQUENCE OF 30-59 AND 92-131.
RC SPECIES=Pig;

RX MEDLINE=90370867; PubMed=2395872;
RA Gafvelin G., Joernvall H., Mutt V.;
RT "Processing of prosecretin: isolation of a secretin precursor from
RT porcine intestine.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6781-6785(1990).
RN [5]
RP SYNTHESIS OF 30-131.
RC SPECIES=Pig;
RX MEDLINE=67244720; PubMed=5978238;
RA Bodanszky M., Ondetti M.A., Levine S.D., Narayanan V.L.,
RA Von Saltza M., Sheehan J.T., Williams N.J., Sabo E.F.;
RT "Synthesis of a heptacosapeptide amide with the hormonal activity of
RT secretin.";
RL Chem. Ind. 42:1757-1758(1966).
RN [6]
RP SEQUENCE OF 30-56.
RC SPECIES=Bovine;
RX MEDLINE=81237102; PubMed=7250377;
RA Carlquist M., Joernvall H., Mutt V.;
RT "Isolation and amino acid sequence of bovine secretin.";
RL FEBS Lett. 127:71-74(1981).
RN [7]
RP SEQUENCE OF 30-56.
RC SPECIES=C.porcellus;
RX MEDLINE=90254163; PubMed=2340294;
RA Buscaill L., Cauvin A., Gourlet P., Gossen D., de Neef P., Rathe J.,
RA Robberecht P., Vandermeers-Piret M.-C., Vandermeers A., Christophe J.;
RT "Purification and amino acid sequence of vasoactive intestinal
RT peptide, peptide histidine isoleucinamide (1-27) and secretin from
RT the small intestine of guinea pig.";
RL Biochim. Biophys. Acta 1038:355-359(1990).
RN [8]
RP STRUCTURE BY NMR OF SECRETIN.
RX MEDLINE=88151942; PubMed=2831051;
RA Clore G.M., Nilges M., Bruenger A., Gronenborn A.M.;
RT "Determination of the backbone conformation of secretin by restrained
RT molecular dynamics on the basis of interproton distance data.";
RL Eur. J. Biochem. 171:479-484(1988).
RN [9]
RP STRUCTURE BY NMR OF SECRETIN.
RX MEDLINE=87191017; PubMed=2883029;
RA Gronenborn A.M., Bovermann G., Clore G.M.;
RT "A 1H-NMR study of the solution conformation of secretin. Resonance
RT assignment and secondary structure.";
RL FEBS Lett. 215:88-94(1987).
CC -!- FUNCTION: STIMULATES FORMATION OF NAHCO(3)-RICH PANCREATIC JUICE
CC AND SECRETION OF NAHCO(3)-RICH BILE AND INHIBITS HCL PRODUCTION
CC BY THE STOMACH.
CC -!- PHARMACEUTICAL: Available under the name Secretin-Ferring (Ferring
CC Pharmaceuticals).
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
CC -----
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CC -----
DR EMBL; M31496; AAA31121.1; -.
DR PIR; B35094; SEPG.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Hormone; Amidation;
KW Cleavage on pair of basic residues; Signal; Pharmaceutical.
FT NON_TER 1 1
FT SIGNAL <1 18
FT PEPTIDE 30 56 SECRETIN.
FT MOD_RES 56 56 AMIDATION (G-57 PROVIDE AMIDE GROUP).
SQ SEQUENCE 131 AA; 14277 MW; 1A24BDDA600E4E34 CRC64;

Query Match 93.2%; Score 123; DB 1; Length 131;
Best Local Similarity 92.6%; Pred. No. 1.7e-11;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|||:|||||:|||||
Db 30 HSDGTFTSELSRLRDSARLQRLLQGLV 56

RESULT 5

SECR_RAT

ID SECR_RAT STANDARD; PRT; 134 AA.
AC P11384;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Secretin precursor.
GN SCT.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90192795; PubMed=2315322;
RA Kopin A.S., Wheeler M.B., Leiter A.B.;
RT "Secretin: structure of the precursor and tissue distribution of the mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:2299-2303 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91271384; PubMed=1711228;
RA Kopin A.S., Wheeler M.B., Nishitani J., McBride E.W., Chang T.M.,
RA Chey W.Y., Leiter A.B.;
RT "The secretin gene: evolutionary history, alternative splicing, and
developmental regulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5335-5339 (1991).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

RX MEDLINE=91286291; PubMed=2061329;
 RA Itoh N., Furuya T., Ozaki K., Kawasaki T.;
 RT "The secretin precursor gene. Structure of the coding region and
 expression in the brain.";
 RL J. Biol. Chem. 266:12595-12598 (1991).
 RN [4]
 RP SEQUENCE OF 33-59.
 RX MEDLINE=89246545; PubMed=2719704;
 RA Gossen D., Vandermeers A., Vandermeers-Piret M.-C., Rathe J.,
 RA Cauvin A., Robberecht P., Christophe J.;
 RT "Isolation and primary structure of rat secretin.";
 RL Biochem. Biophys. Res. Commun. 160:862-867 (1989).
 CC -!- FUNCTION: STIMULATES FORMATION OF NAHCO(3)-RICH PANCREATIC JUICE
 CC AND SECRETION OF NAHCO(3)-RICH BILE AND INHIBITS HCL PRODUCTION
 CC BY THE STOMACH.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
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 CC -----
 DR EMBL; M31495; AAA42126.1; -.
 DR EMBL; M64033; AAA42128.1; -.
 DR EMBL; M63984; AAA42127.1; -.
 DR PIR; A40886; A40959.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Hormone; Amidation;
 KW Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT PEPTIDE 33 59 SECRETIN.
 FT MOD_RES 59 59 AMIDATION (G-60 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 134 AA; 15072 MW; D9FA1A4C1F7C86E6 CRC64;

 Query Match 90.2%; Score 119; DB 1; Length 134;
 Best Local Similarity 88.9%; Pred. No. 7e-11;
 Matches 24; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
 |||||||:: |||||
 Db 33 HSDGTFTSELSRLQDSARLQRLLQGLV 59

RESULT 6
 SECR_MOUSE
 ID SECR_MOUSE STANDARD; PRT; 133 AA.
 AC Q08535;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Secretin precursor.

GN SCT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94234995; PubMed=8179583;
 RA Lan M.S., Kajiyama W., Donadel G., Lu J., Notkins A.L.;
 RT "cDNA sequence and genomic organization of mouse secretin.";
 RL Biochem. Biophys. Res. Commun. 200:1066-1071(1994).
 CC -!- FUNCTION: STIMULATES FORMATION OF NAHCO(3)-RICH PANCREATIC JUICE
 CC AND SECRETION OF NAHCO(3)-RICH BILE AND INHIBITS HCL PRODUCTION
 CC BY THE STOMACH.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 CC -----
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 CC -----
 DR EMBL; U07568; AAA18453.1; -.
 DR EMBL; X73580; CAA51982.1; -.
 DR PIR; JC2202; JC2202.
 DR MGD; MGI:99466; Sct.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Hormone; Amidation;
 KW Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 22 BY SIMILARITY.
 FT PEPTIDE 32 58 SECRETIN (BY SIMILARITY).
 FT MOD_RES 58 58 AMIDATION (G-59 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 133 AA; 14914 MW; 9B69CBCF74CA9709 CRC64;

 Query Match 85.6%; Score 113; DB 1; Length 133;
 Best Local Similarity 85.2%; Pred. No. 5.6e-10;
 Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

 Qy 1 HSDGTFTSELSRLREGARLQRLQQGLV 27
 ||||| |||||||||:: |||||||||
 Db 32 HSDGMFTSELSRLQDSARLQRLQQGLV 58

RESULT 7
 SECR_RABIT
 ID SECR_RABIT STANDARD; PRT; 27 AA.
 AC P32647;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Secretin.
 GN SCT.

OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Small intestine;
RX MEDLINE=90259845; PubMed=2342988;
RA Gossen D., Buscail L., Cauvin A., Gourlet P., de Neef P., Rathe J.,
RA Robberecht P., Vandermeers-Piret M.C., Vandermeers A., Christophe J.;
RT "Amino acid sequence of VIP, PHI and secretin from the rabbit small
RT intestine.";
RL Peptides 11:123-128(1990).
CC -!- FUNCTION: STIMULATES FORMATION OF NAHCO(3)-RICH PANCREATIC JUICE
CC AND SECRETION OF NAHCO(3)-RICH BILE AND INHIBITS HCL PRODUCTION
CC BY THE STOMACH.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR; C60415; C60415.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Hormone; Amidation.
FT MOD_RES 27 27 AMIDATION.
SQ SEQUENCE 27 AA; 3105 MW; 38A015800BDD3618 CRC64;

Query Match 84.8%; Score 112; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 1.4e-10;
Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||| ||||| : ||||| :
Db 1 HSDGTLTSELSRLDRARLQRLLQGLL 27

RESULT 8
SECR_CHICK
ID SECR_CHICK STANDARD; PRT; 27 AA.
AC P01280;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Secretin.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=81114197; PubMed=7460928;
RA Nilsson A., Carlquist M., Joernvall H., Mutt V.;
RT "Isolation and characterization of chicken secretin.";
RL Eur. J. Biochem. 112:383-388(1980).
CC -!- FUNCTION: STIMULATES FORMATION OF NAHCO(3)-RICH PANCREATIC JUICE
CC AND SECRETION OF NAHCO(3)-RICH BILE AND INHIBITS HCL PRODUCTION
CC BY THE STOMACH.

CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR; A01545; SECH.
DR HSSP; P01275; 1BH0.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Hormone; Amidation.
FT MOD_RES 27 27 AMIDATION.
SQ SEQUENCE 27 AA; 3131 MW; DA0AD71B6361BE7E CRC64;

Query Match 59.1%; Score 78; DB 1; Length 27;
Best Local Similarity 51.9%; Pred. No. 1.8e-05;
Matches 14; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
| | | | | | | : : | | : | : | : | : |
Db 1 HSDGLFTSEYSKMRGNAQVQKFIQNLM 27

RESULT 9
EXE1_HELSU
ID EXE1_HELSU STANDARD; PRT; 38 AA.
AC P04203;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Exendin-1 (Helospectins I and II).
OS Heloderma suspectum (Gila monster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;
OC Heloderma.
OX NCBI_TaxID=8554;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=85006896; PubMed=6207171;
RA Parker D.S., Raufman J.-P., O'Donohue T.L., Bledsoe M., Yoshida H.,
RA Pisano J.J.;
RT "Amino acid sequences of helospectins, new members of the glucagon
superfamily, found in Gila monster venom.";
RL J. Biol. Chem. 259:11751-11755(1984).
CC -!- FUNCTION: Has a VIP/secretin-like biological activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Toxin.
FT VARIANT 38 38 MISSING (IN HELOSPECTIN II).
SQ SEQUENCE 38 AA; 4096 MW; 54275BCFC368314A CRC64;

Query Match 46.2%; Score 61; DB 1; Length 38;
Best Local Similarity 44.4%; Pred. No. 0.0091;
Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HSDGIFTSELSRLREGARLQRLLQGLV 27
||| |||:| |::| ||: |: ::
Db 1 HSDATFTAESKLLAKLALQKYLESL 27

RESULT 10
GLUC_CAVPO
ID GLUC_CAVPO STANDARD; PRT; 180 AA.
AC P05110;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucagon precursor [Contains: Glicentin-related polypeptide (GRPP);
DE Glucagon; Glucagon-37 (Oxyntomodulin); Glucagon-like peptide 1 (GLP1);
DE Glucagon-like peptide 2 (GLP2)].
GN GCG.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86248118; PubMed=3755107;
RA Seino S., Welsh M., Bell G.I., Chan S.J., Steiner D.F.;
RT "Mutations in the guinea pig preproglucagon gene are restricted to a
RT specific portion of the prohormone sequence.";
RL FEBS Lett. 203:25-30(1986).
RN [2]
RP SEQUENCE OF 53-81.
RX MEDLINE=86165412; PubMed=3956884;
RA Huang C.G., Eng J., Pan Y.-C.E., Hulmes J.D., Yalow R.S.;
RT "Guinea pig glucagon differs from other mammalian glucagons.";
RL Diabetes 35:508-512(1986).
RN [3]
RP PARTIAL SEQUENCE OF 53-89.
RX MEDLINE=86017849; PubMed=4048553;
RA Conlon J.M., Hansen H.F., Schwartz T.W.;
RT "Primary structure of glucagon and a partial sequence of
RT oxyntomodulin (glucagon-37) from the guinea pig.";
RL Regul. Pept. 11:309-320(1985).
CC -!- FUNCTION: GLUCAGON PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND
CC RAISES THE BLOOD SUGAR LEVEL.
CC -!- FUNCTION: GLP2 STIMULATES INTESTINAL GROWTH AND UPREGULATES VILLUS
CC HEIGHT IN THE SMALL INTESTINE, CONCOMITANT WITH INCREASED CRYPT
CC CELL PROLIFERATION AND DECREASED ENTEROCYTE APOPTOSIS.
CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
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DR EMBL; D00014; BAA00010.1; -.
DR PIR; A24856; GCGP.
DR HSSP; P01274; 1GCN.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 3.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 3.
DR PROSITE; PS00260; GLUCAGON; 4.
KW Glucagon family; Hormone; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 20
FT PEPTIDE 21 50 GLICENTIN-RELATED POLYPEPTIDE.
FT PEPTIDE 53 81 GLUCAGON.
FT PEPTIDE 53 89 GLUCAGON-37.
FT PEPTIDE 92 128 GLUCAGON-LIKE PEPTIDE 1.
FT PROPEP 131 143
FT PEPTIDE 146 178 GLUCAGON-LIKE PEPTIDE 2.
SQ SEQUENCE 180 AA; 20972 MW; 702FB181161D2776 CRC64;

Query Match 46.2%; Score 61; DB 1; Length 180;
Best Local Similarity 44.4%; Pred. No. 0.049;
Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|| |||||: |: : | |: |: |:
Db 53 HSQGTFTSDYSKYLDSRRAQQFLKWLL 79

RESULT 11
EXE3_HELHO
ID EXE3_HELHO STANDARD; PRT; 39 AA.
AC P20394;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Exendin-3.
OS Heloderma horridum horridum (Mexican beaded lizard).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;
OC Heloderma.
OX NCBI_TaxID=8552;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=91056067; PubMed=1700785;
RA Eng J., Andrew P.C., Kleinman W.A., Singh L., Raufman J.-P.;
RT "Purification and structure of exendin-3, a new pancreatic
secretagogue isolated from Heloderma horridum venom.";
RL J. Biol. Chem. 265:20259-20262(1990).
CC -!- FUNCTION: Has a VIP/secretin-like biological activity. Interacts
with the exendin receptor.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR; A23674; HWGH3Z.
DR HSSP; P01275; 1BH0.
DR InterPro; IPR000532; Glucagon.

DR Pfam; PF00123; hormone2; 1.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Toxin; Amidation.
FT MOD_RES 39 39 AMIDATION.
SQ SEQUENCE 39 AA; 4204 MW; A44251D3A4B1D1B9 CRC64;

Query Match 45.5%; Score 60; DB 1; Length 39;
Best Local Similarity 46.2%; Pred. No. 0.013;
Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGL 26
|||:|||:||:| :: :: |
Db 1 HSDGTFTSDLSKQMEEEAVRLFIEWL 26

RESULT 12
GLUC_DIDMA
ID GLUC_DIDMA STANDARD PRT; 29 AA.
AC P18108;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucagon.
GN GCG.
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=90160042; PubMed=2695899;
RA Yu J.-H., Eng J., Rattan S., Yalow R.S.;
RT "Opossum insulin, glucagon and pancreatic polypeptide: amino acid
RT sequences.";
RL Peptides 10:1195-1197(1989).
CC -!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
CC THE BLOOD SUGAR LEVEL.
CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR; JQ0364; GCOPV.
DR HSSP; P01274; 1GCN.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Hormone.
SQ SEQUENCE 29 AA; 3456 MW; 04D474D35C752B27 CRC64;

Query Match 44.7%; Score 59; DB 1; Length 29;
Best Local Similarity 44.4%; Pred. No. 0.014;
Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27

Db || || |||: | : | | :| |:
1 HSQGTFTSDYSKYLDSRRAQDFVQWLM 27

RESULT 13

GLUC_RABIT

ID GLUC_RABIT STANDARD; PRT; 29 AA.
AC P25449;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Glucagon.
GN GCG.
OS Oryctolagus cuniculus (Rabbit),
OS Camelus dromedarius (Dromedary) (Arabian camel), and
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986, 9838, 9521;
RN [1]
RP SEQUENCE.
RC SPECIES=Rabbit;
RX MEDLINE=72129389; PubMed=5011077;
RA Sundby F., Markussen J.;
RT "Rabbit glucagon: isolation, crystallization and amino acid
RT composition.";
RL Horm. Metab. Res. 4:56-56(1972).
RN [2]
RP SEQUENCE.
RC SPECIES=C.dromedarius;
RX MEDLINE=75027473; PubMed=4421675;
RA Sundby F., Markussen J., Danho W.;
RT "Camel glucagon: isolation, crystallization and amino acid
RT composition.";
RL Horm. Metab. Res. 6:425-425(1974).
RN [3]
RP SEQUENCE.
RC SPECIES=S.sciureus; TISSUE=Pancreas;
RX MEDLINE=91088593; PubMed=2263627;
RA Yu J.-H., Eng J., Yalow R.S.;
RT "Isolation and amino acid sequences of squirrel monkey (Saimiri
RT sciurea) insulin and glucagon.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:9766-9768(1990).
CC -!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
CC THE BLOOD SUGAR LEVEL.
CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR; A91741; A91741.
DR PIR; A91742; A91742.
DR PIR; C39258; C39258.
DR HSSP; P01274; 1GCN.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.

KW Glucagon family; Hormone.
 SQ SEQUENCE 29 AA; 3483 MW; 04C584D35C752B27 CRC64;
 Query Match 44.7%; Score 59; DB 1; Length 29;
 Best Local Similarity 44.4%; Pred. No. 0.014;
 Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 QY 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
 || |||||: | : | | : | |:
 Db 1 HSQGTFTSDYSKYLDSRRAQDFVQWLM 27

RESULT 14

GLUC_CANFA

ID GLUC_CANFA STANDARD; PRT; 69 AA.
 AC P29794;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glucagon precursor [Contains: Glicentin; Glicentin-related polypeptide (GRPP); Glucagon; Glucagon-37 (Oxyntomodulin)] (Fragment).
 GN GCG.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Ileum;
 RX MEDLINE=89185675; PubMed=3238052;
 RA Shinomura Y., Eng J., Yalow R.S.;
 RT "Immunoreactive glucagons purified from dog pancreas, stomach and ileum."
 RL Regul. Pept. 23:299-308 (1988).
 CC -!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.
 CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; A60318; GCDG69.
 DR HSSP; P01274; 1GCN.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Hormone; Cleavage on pair of basic residues.
 FT NON_TER 1 1
 FT PEPTIDE 1 69 GLICENTIN.
 FT PEPTIDE 1 30 GLICENTIN-RELATED POLYPEPTIDE.
 FT PEPTIDE 33 61 GLUCAGON.
 FT PEPTIDE 33 69 GLUCAGON-37.
 SQ SEQUENCE 69 AA; 8170 MW; 385BE30BDAED86E1 CRC64;

Query Match 44.7%; Score 59; DB 1; Length 69;
 Best Local Similarity 44.4%; Pred. No. 0.035;
 Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
 || |||||: |: : | | :| |:
Db 33 HSQGTFTSDYSKYLDSRRAQDFVQWLM 59

RESULT 15

GLUC_RANCA

ID GLUC_RANCA STANDARD; PRT; 103 AA.
AC P15438; P15439; P15440;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Glucagon precursor (Fragments).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=88257102; PubMed=3260236;
RA Pollock H.G., Hamilton J.W., Rouse J.B., Ebner K.E., Rawitch A.B.;
RT "Isolation of peptide hormones from the pancreas of the bullfrog
RT (Rana catesbeiana). Amino acid sequences of pancreatic polypeptide,
RT oxyntomodulin, and two glucagon-like peptides.";
RL J. Biol. Chem. 263:9746-9751(1988).
CC -!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
CC THE BLOOD SUGAR LEVEL.
CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
CC -!- MISCELLANEOUS: X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH
CC OTHER SPECIES SEQUENCES.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR HSSP; P01274; 1GCN.
DR InterPro; IPR000532; Glucagon.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 3.
DR PROSITE; PS00260; GLUCAGON; 3.
KW Glucagon family; Hormone.
FT PEPTIDE 1 29 GLUCAGON.
FT PEPTIDE 1 36 GLUCAGON-36 (OXYNTOMODULIN).
FT PEPTIDE 39 70 GLUCAGON-LIKE PEPTIDE 1.
FT NON_CONS 70 71
FT PEPTIDE 71 103 GLUCAGON-LIKE PEPTIDE 2.
SQ SEQUENCE 103 AA; 11719 MW; 316287B7BAE1C8F7 CRC64;

Query Match 44.7%; Score 59; DB 1; Length 103;
Best Local Similarity 44.4%; Pred. No. 0.054;
Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
 || |||||: |: : | | :| |:
Db 1 HSQGTFTSDYSKYLDSRRAQDFVQWLM 27

Job time : 12 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2003, 18:07:22 ; Search time 22 Seconds
(without alignments)
118.025 Million cell updates/sec

Title: US-09-897-412-10
Perfect score: 132
Sequence: 1 HSDGTFTSELSRLREGARLQRLLQGLV 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query			SUMMARIES	
		Match	Length	DB	ID	Description
1	132	100.0	27	1	S07443	secretin - human
2	126	95.5	27	2	A27267	secretin - dog
3	123	93.2	27	1	SEBO	secretin - bovine
4	123	93.2	27	1	SESH	secretin - sheep
5	123	93.2	131	1	SEPG	secretin precursor
6	119	90.2	134	2	A40959	secretin precursor
7	115	87.1	26	1	B57082	secretin - guinea
8	113	85.6	133	2	JC2202	secretin precursor
9	112	84.8	27	2	C60415	secretin - rabbit
10	78	59.1	27	1	SECH	secretin - chicken
11	67	50.8	258	2	G83069	probable oxidoredu
12	61	46.2	38	1	HWGHS	exendin-1 - Mexica
13	61	46.2	180	1	GCGP	glucagon precursor

14	60	45.5	39	1	HWGH3Z	exendin-3 - Mexica
15	59	44.7	29	1	GCOPV	glucagon - North A
16	59	44.7	29	2	A91740	glucagon - turkey
17	59	44.7	29	2	A91741	glucagon - rabbit
18	59	44.7	29	2	A91742	glucagon - Arabian
19	59	44.7	29	2	C39258	glucagon - common
20	59	44.7	36	2	D60840	glucagon II - Euro
21	59	44.7	69	1	GCDG69	glucagon-69 - dog
22	59	44.7	101	1	GCFGB	glucagon precursor
23	59	44.7	151	1	GCCH	glucagon precursor
24	59	44.7	158	1	GCPG	glucagon precursor
25	59	44.7	180	1	GCHU	glucagon precursor
26	59	44.7	180	1	GCRT	glucagon precursor
27	59	44.7	180	1	GCHY	glucagon precursor
28	59	44.7	180	1	GCBO	glucagon precursor
29	59	44.7	180	2	A57294	glucagon precursor
30	59	44.7	206	2	I51301	proglucagon - chic
31	58	43.9	29	1	GCDF	glucagon - smaller
32	57	43.2	29	1	GCDK	glucagon - duck
33	57	43.2	29	1	A61583	glucagon - ostrich
34	57	43.2	29	1	GCTTS	glucagon - slider
35	57	43.2	29	2	S07211	glucagon - marbled
36	57	43.2	29	2	C60840	glucagon I - Europ
37	57	43.2	55	1	VRRB	vasoactive intesti
38	57	43.2	58	1	VRPG	vasoactive intesti
39	56	42.4	55	1	VRBO	vasoactive intesti
40	56	42.4	55	1	VRSH	vasoactive intesti
41	56	42.4	55	1	VRGP	vasoactive intesti
42	56	42.4	170	1	VRRT	vasoactive intesti
43	56	42.4	170	2	A60037	vasoactive intesti
44	56	42.4	180	1	GCRTDU	glucagon precursor
45	55	41.7	29	2	S39018	glucagon - bowfin

ALIGNMENTS

RESULT 1

S07443

secretin - human

C;Species: Homo sapiens (man)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: S07443

R;Carlquist, M.; Joernvall, H.; Forssmann, W.G.; Thulin, L.; Johansson, C.; Mutt, V.

IRCS Med. Sci. 13, 217-218, 1985

A;Title: Human secretin is not identical to the porcine/bovine hormone.

A;Reference number: S07443

A;Accession: S07443

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-27 <CAR>

C;Genetics:

A;Gene: GDB:SCT

A;Cross-references: GDB:270550

A;Map position: Xp21.1-Xp21.1

C;Superfamily: glucagon

C;Keywords: amidated carboxyl end; duplication
F;27/Modified site: amidated carboxyl end (Val) #status predicted

Query Match 100.0%; Score 132; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
| | | | | | | | | | | | | | | | | | | | | |
Db 1 HSDGTFTSELSRLREGARLQRLLQGLV 27

RESULT 2
A27267
secretin - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 21-Nov-1997
C;Accession: A27267
R;Shinomura, Y.; Eng, J.; Yallow, R.S.
Life Sci. 41, 1243-1248, 1987
A;Title: Dog secretin: sequence and biologic activity.
A;Reference number: A27267; MUID:87314204; PMID:3626755
A;Accession: A27267
A;Molecule type: protein
A;Residues: 1-27 <SHI>
A;Experimental source: intestine
C;Superfamily: glucagon
C;Keywords: duplication

Query Match 95.5%; Score 126; DB 2; Length 27;
Best Local Similarity 96.3%; Pred. No. 9.7e-13;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
| | | | | | | | | | | | | | | | | | | | | |
Db 1 HSDGTFTSELSRLRESARLQRLLQGLV 27

RESULT 3
SEBO
secretin - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Mar-1998
C;Accession: A91291; A01544
R;Carlquist, M.; Jornvall, H.; Mutt, V.
FEBS Lett. 127, 71-74, 1981
A;Title: Isolation and amino acid sequence of bovine secretin.
A;Reference number: A91291; MUID:81237102; PMID:7250377
A;Accession: A91291
A;Molecule type: protein
A;Residues: 1-27 <CAR>
C;Superfamily: glucagon
C;Keywords: amidated carboxyl end; duodenal mucosa; duplication; hormone;
secretagogue
F;27/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 93.2%; Score 123; DB 1; Length 27;

Best Local Similarity 92.6%; Pred. No. 2.8e-12;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|||: |||||
Db 1 HSDGTFTSELSRLRDSARLQRLLQGLV 27

RESULT 4

SESH

secretin - sheep

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 20-Mar-1998
C;Accession: C60072
R;Bounjoua, Y.; Vandermeers, A.; Robberecht, P.; Vandermeers-Piret, M.C.;
Christophe, J.
Regul. Pept. 32, 169-179, 1991
A;Title: Purification and amino acid sequence of vasoactive intestinal peptide,
peptide histidine isoleucinamide and secretin from the ovine small intestine.
A;Reference number: A60072; MUID:91239834; PMID:2034821
A;Accession: C60072
A;Molecule type: protein
A;Residues: 1-27 <BOU>
C;Superfamily: glucagon
C;Keywords: amidated carboxyl end; duplication; hormone; intestine
F;27/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 93.2%; Score 123; DB 1; Length 27;
Best Local Similarity 92.6%; Pred. No. 2.8e-12;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|||: |||||
Db 1 HSDGTFTSELSRLRDSARLQRLLQGLV 27

RESULT 5

SEPG

secretin precursor - pig

C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
C;Accession: B35094; A01544; A36052
R;Kopin, A.S.; Wheeler, M.B.; Leiter, A.B.
Proc. Natl. Acad. Sci. U.S.A. 87, 2299-2303, 1990
A;Title: Secretin: structure of the precursor and tissue distribution of the mRNA.
A;Reference number: A35094; MUID:90192795; PMID:2315322
A;Accession: B35094
A;Molecule type: mRNA
A;Residues: 1-131 <KOP>
A;Cross-references: GB:M31496; NID:g164670; PIDN:AAA31121.1; PID:g164671
R;Mutt, V.; Jorpes, J.E.; Magnusson, S.
Eur. J. Biochem. 15, 513-519, 1970
A;Title: Structure of porcine secretin. The amino acid sequence.
A;Reference number: A91147; MUID:70282334; PMID:5465996
A;Accession: A01544
A;Molecule type: protein

A;Residues: 30-56 < MUT >
A;Note: tryptic peptides were sequenced
R;Gafvelin, G.; Joernvall, H.; Mutt, V.
Proc. Natl. Acad. Sci. U.S.A. 87, 6781-6785, 1990
A;Title: Processing of prosecretin: isolation of a secretin precursor from porcine intestine.
A;Reference number: A36052; MUID:90370867; PMID:2395872
A;Accession: A36052
A;Status: preliminary
A;Molecule type: protein
A;Residues: 30-59, 'R', 92-131 < GAF >
R;Bodanszky, M.; Ondetti, M.A.; Levine, S.D.; Narayanan, V.L.; Saltza, M.V.; Sheehan, J.T.; Williams, N.J.; Sabo, E.F.
Chem. Ind. 1966, 1757-1758, 1966
A;Title: Synthesis of a heptacosapeptide amide with the hormonal activity of secretin.
A;Reference number: A90916
A;Contents: annotation
A;Note: synthesis confirmed the proposed structure of the natural hormone
C;Superfamily: glucagon
C;Keywords: amidated carboxyl end; duodenal mucosa; duplication; hormone; secretagogue
F;1-18/Domain: signal sequence #status predicted < SIG >
F;30-56/Product: secretin #status experimental < MAT >
F;56/Modified site: amidated carboxyl end (Val) (amide in mature form from following glycine) #status experimental

Query Match 93.2%; Score 123; DB 1; Length 131;
Best Local Similarity 92.6%; Pred. No. 1.7e-11;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|||: |||: |||
Db 30 HSDGTFTSELSRLRDSARLQRLLQGLV 56

RESULT 6
A40959
secretin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 16-Jul-1999
C;Accession: A40886; A40959; A35094; A32544
R;Itoh, N.; Furuya, T.; Ozaki, K.; Ohta, M.; Kawasaki, T.
J. Biol. Chem. 266, 12595-12598, 1991
A;Title: The secretin precursor gene. Structure of the coding region and expression in the brain.
A;Reference number: A40886; MUID:91286291; PMID:2061329
A;Accession: A40886
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-134 < ITO >
A;Cross-references: GB:M63984; NID:g206889; PIDN:AAA42127.1; PID:g206890
R;Kopin, A.S.; Wheeler, M.B.; Nishitani, J.; McBride, E.W.; Chang, T.; Chey, W.Y.; Leiter, A.B.
Proc. Natl. Acad. Sci. U.S.A. 88, 5335-5339, 1991
A;Title: The secretin gene: evolutionary history, alternative splicing, and developmental regulation.

A;Reference number: A40959; MUID:91271384; PMID:1711228
A;Accession: A40959
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-134 <KOP>
A;Cross-references: GB:M64033; NID:g206891; PIDN:AAA42128.1; PID:g206892
R;Kopin, A.S.; Wheeler, M.B.; Leiter, A.B.
Proc. Natl. Acad. Sci. U.S.A. 87, 2299-2303, 1990
A;Title: Secretin: structure of the precursor and tissue distribution of the mRNA.
A;Reference number: A35094; MUID:90192795; PMID:2315322
A;Accession: A35094
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-134 <KOP2>
A;Cross-references: GB:M31495; NID:g206887; PIDN:AAA42126.1; PID:g206888
R;Gossen, D.; Vandermeers, A.; Vandermeers-Piret, M.C.; Rathe, J.; Cauvin, A.;
Robberecht, P.; Christophe, J.
Biochem. Biophys. Res. Commun. 160, 862-867, 1989
A;Title: Isolation and primary structure of rat secretin.
A;Reference number: A32544; MUID:89246545; PMID:2719704
A;Accession: A32544
A;Status: preliminary
A;Molecule type: protein
A;Residues: 33-59 <GOS>
C;Superfamily: glucagon
C;Keywords: duplication

Query Match 90.2%; Score 119; DB 2; Length 134;
Best Local Similarity 88.9%; Pred. No. 7e-11;
Matches 24; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|||:|||||:: |||||:|||
Db 33 HSDGTFTSELSRLQDSARLQRLLQGLV 59

RESULT 7
B57082
secretin - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: B57082
R;Buscail, L.; Cauvin, A.; Gourlet, P.; Gossen, D.; de Neef, P.; Rathe, J.;
Robberecht, P.; Vandermeers-Piret, M.C.; Vandermeers, A.; Christophe, J.
Biochim. Biophys. Acta 1038, 355-359, 1990
A;Title: Purification and amino acid sequence of vasoactive intestinal peptide,
peptide histidine isoleucinamide (1-27) and secretin from the small intestine of
guinea pig.
A;Reference number: S09688; MUID:90254163; PMID:2340294
A;Accession: B57082
A;Molecule type: protein
A;Residues: 1-26 <BUS>
C;Superfamily: glucagon
C;Keywords: amidated carboxyl end; duodenal mucosa; duplication; hormone;
secretagogue
F;1-26/Product: secretin #status experimental <MAT>

F;26/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 87.1%; Score 115; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 4.5e-11;
Matches 24; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SDGTFTSELSRLREGARLQRLLQGLV 27
||| ||||| | : ||| |||||
Db 1 SDGTFTSELSRLRDSARLQRLLQGLV 26

RESULT 8

JC2202

secretin precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 16-Jul-1999

C;Accession: JC2202; S34214

R;Lan, M.S.; Kajiyama, W.; Donadel, G.; Lu, J.; Notkins, A.L.

Biochem. Biophys. Res. Commun. 200, 1066-1071, 1994

A;Title: cDNA sequence and genomic organization of mouse secretin.

A;Reference number: JC2202; MUID:94234995; PMID:8179583

A;Accession: JC2202

A;Molecule type: mRNA

A;Residues: 1-133 <LAN>

A;Cross-references: EMBL:X73580; NID:g313710; PIDN:CAA51982.1; PID:g313711

C;Comment: This protein regulates the secretion of pancreatic juices and stimulates insulin secretion.

C;Superfamily: glucagon

C;Keywords: amidated carboxyl end; duplication; hormone; secretagogue

F;1-27/Domain: signal sequence #status predicted <SIG>

F;28-133/Product: prosecretin #status predicted <PRO>

F;32-58/Product: secretin #status predicted <MAT>

F;58/Modified site: amidated carboxyl end (Val) (amide in mature form from following glycine) #status predicted

Query Match 85.6%; Score 113; DB 2; Length 133;
Best Local Similarity 85.2%; Pred. No. 5.8e-10;
Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27

|||| | | | | | | | : | | | | | | |

Db 32 HSDGMFTSELSRLQDSARLQRLLQGLV 58

RESULT 9

C60415

secretin - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 20-Mar-1998

C;Accession: C60415

R;Gossem, D.; Buscail, L.; Cauvin, A.; Gourlet, P.; De Neef, P.; Rathe, J.; Robberecht, P.; Vandermeers-Piret, M.C.; Vandermeers, A.; Christophe, J. Peptides 11, 123-128, 1990

A;Title: Amino acid sequence of VIP, PHI and secretin from the rabbit small intestine.

A;Reference number: A60415; MUID:90259845; PMID:2342988

A;Accession: C60415

A;Molecule type: protein
A;Residues: 1-27 <GOS>
C;Superfamily: glucagon
C;Keywords: amidated carboxyl end; duplication; hormone; intestine; secretagogue
F;27/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 84.8%; Score 112; DB 2; Length 27;
Best Local Similarity 85.2%; Pred. No. 1.4e-10;
Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||| ||| | : | ||| ||| : |
Db 1 HSDGTLTSELSRLDRARLQRLLQGLL 27

RESULT 10

SECH
secretin - chicken
C;Species: Gallus gallus (chicken)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Nov-1997
C;Accession: A01545
R;Nilsson, A.; Carlquist, M.; Jornvall, H.; Mutt, V.
Eur. J. Biochem. 112, 383-388, 1980
A;Title: Isolation and characterization of chicken secretin.
A;Reference number: A01545; MUID:81114197; PMID:7460928
A;Accession: A01545
A;Molecule type: protein
A;Residues: 1-27 <NIL>
C;Superfamily: glucagon
C;Keywords: amidated carboxyl end; duplication; hormone
F;27/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 59.1%; Score 78; DB 1; Length 27;
Best Local Similarity 51.9%; Pred. No. 2.3e-05;
Matches 14; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||| ||| | : | | : | : | : |
Db 1 HSDGLFTSEYSKMRGNQVKFIQNL 27

RESULT 11

G83069
probable oxidoreductase PA4615 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: G83069
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brinkman, F.S.L.; Hufnagle, W.O.; Kowalik, D.J.; Lagrou, M.; Garber, R.L.; Goltry, L.; Tolentino, E.; Westbrook-Wadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, R.M.; Smith, K.A.; Spencer, D.H.; Wong, G.K.S.; Wu, Z.; Paulsen, I.T.; Reizer, J.; Saier, M.H.; Hancock, R.E.W.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.
A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: G83069
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <STO>
A;Cross-references: GB:AE004875; GB:AE004091; NID:g9950857; PIDN:AAG08003.1;
GSPDB:GN00131; PASP:PA4615
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA4615

Query Match 50.8%; Score 67; DB 2; Length 258;
Best Local Similarity 82.4%; Pred. No. 0.014;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DGTFTSELSRLREGARL 19
|| ||||||| :|
Db 78 DGEFTSELSRLREGDQL 94

RESULT 12

HWGHS

exendin-1 - Mexican beaded lizard

N;Alternate names: helodermin H38; helospectin I

N;Contains: helospectin II

C;Species: Heloderma horridum (Mexican beaded lizard)

C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 07-May-1999

C;Accession: A01555

R;Parker, D.S.; Raufman, J.P.; O'Donohue, T.L.; Bledsoe, M.; Yoshida, H.; Pisano, J.J.

J. Biol. Chem. 259, 11751-11755, 1984

A;Title: Amino acid sequences of helospectins, new members of the glucagon superfamily, found in Gila monster venom.

A;Reference number: A01555; MUID:85006896; PMID:6207171

A;Note: Heloderma suspectum (Gila monster)

A;Accession: A01555

A;Molecule type: protein

A;Residues: 1-38 <PAR>

R;Vandermeers, A.; Gourlet, P.; Vandermeers-Piret, M.C.; Cauvin, A.; De Neef, P.; Rathe, J.; Svoboda, M.; Robberecht, P.; Christophe, J.

Eur. J. Biochem. 164, 321-327, 1987

A;Title: Chemical, immunological and biological properties of peptides like vasoactive-intestinal-peptide and peptide-histidine-isoleucinamide extracted from the venom of two lizards (Heloderma horridum and Heloderma suspectum).

A;Reference number: A37584; MUID:87190398; PMID:3569266

A;Contents: annotation

A;Note: reanalysis of peptide components in the venoms of Heloderma horridum and H. suspectum indicated that exendin-1 and its 37-residue variant are the major components of H. horridum venom, whereas exendin-2 is the major peptide from H. suspectum venom (very small amounts of exendin-1 may be present); it is suggested that the source of the venom used by Parker et al. (reference number A01555) may have been misidentified

C;Comment: Exendins are venom components that are thought to bind to receptors for vasoactive intestinal peptide and/or secretin on pancreatic acinar cells and to activate adenylate cyclase, resulting in secretion of amylase.

C;Superfamily: glucagon

C;Keywords: duplication; secretagogue; venom

F;1-38/Product: exendin-1 (helospectin I) #status experimental <HS1>

F;1-37/Product: helospectin II #status experimental <HS2>

Query Match 46.2%; Score 61; DB 1; Length 38;
Best Local Similarity 44.4%; Pred. No. 0.014;
Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HSDGIFTSELSRLREGARLQRLLQGLV 27
||| |||:| |:| ||: |: ::
Db 1 HSDATFTAEYSKLLAKIALQKYLESIL 27

RESULT 13

GCGP

glucagon precursor - guinea pig

N;Alternate names: oxyntomodulin

N;Contains: glicentin-related peptide; glucagon; glucagon-37 (oxyntomodulin); glucagon-like peptide 1; glucagon-like peptide 2

C;Species: Cavia porcellus (guinea pig)

C;Date: 30-Sep-1987 #sequence_revision 31-Dec-1992 #text_change 16-Jun-2000

C;Accession: A24856; A23849; A60323

R;Seino, S.; Welsh, M.; Bell, G.I.; Chan, S.J.; Steiner, D.F.
FEBS Lett. 203, 25-30, 1986

A;Title: Mutations in the guinea pig preproglucagon gene are restricted to a specific portion of the prohormone sequence.

A;Reference number: A24856; MUID:86248118; PMID:3755107

A;Accession: A24856

A;Molecule type: mRNA

A;Residues: 1-180 <SEI>

A;Cross-references: DDBJ:D00014; GB:N00014; NID:g220288; PIDN:BAA00010.1;
PID:g220289

R;Huang, C.G.; Eng, J.; Pan, Y.C.E.; Hulmes, J.D.; Yalow, R.S.
Diabetes 35, 508-512, 1986

A;Title: Guinea pig glucagon differs from other mammalian glucagons.

A;Reference number: A23849; MUID:86165412; PMID:3956884

A;Accession: A23849

A;Molecule type: protein

A;Residues: 53-81 <HUA>

R;Conlon, J.M.; Hansen, H.F.; Schwartz, T.W.
Regul. Pept. 11, 309-320, 1985

A;Title: Primary structure of glucagon and a partial sequence of oxyntomodulin (glucagon-37) from the guinea pig.

A;Reference number: A60323; MUID:86017849; PMID:4048553

A;Accession: A60323

A;Molecule type: protein

A;Residues: 53-81 <CON>

A;Note: glucagon-37 was not completely sequenced

C;Superfamily: glucagon

C;Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; pancreas

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-180/Product: proglucagon #status predicted <PGC>

F;21-50/Region: glicentin-related peptide #status predicted

F;53-89/Product: glucagon-37 (oxyntomodulin) #status experimental <G37>

F;53-81/Product: glucagon #status experimental <GCN>

F;98-127/Product: glucagon-like peptide 1 #status predicted <GL1>

F;146-178/Product: glucagon-like peptide 2 #status predicted <GL2>

F;127/Modified site: amidated carboxyl end (Arg) (amide in mature form from following glycine) #status predicted

Query Match 46.2%; Score 61; DB 1; Length 180;
Best Local Similarity 44.4%; Pred. No. 0.079;
Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|| |||||: | : : | |: |:
Db 53 HSQGTFTSDYSKYLDSRRAQQFLKWLL 79

RESULT 14

HWGH3Z

exendin-3 - Mexican beaded lizard

C;Species: Heloderma horridum (Mexican beaded lizard)

C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 21-Nov-1997

C;Accession: A23674

R;Eng, J.; Andrews, P.C.; Kleinman, W.A.; Singh, L.; Raufman, J.P.
J. Biol. Chem. 265, 20259-20262, 1990

A;Title: Purification and structure of exendin-3, a new pancreatic secretagogue isolated from Heloderma horridum venom.

A;Reference number: A23674; MUID:91056067; PMID:1700785

A;Accession: A23674

A;Molecule type: protein

A;Residues: 1-39 <ENG>

C;Comment: Exendins are venom components that are thought to bind to receptors for vasoactive intestinal peptide and/or secretin on pancreatic acinar cells and to activate adenylyl cyclase, resulting in secretion of amylase.

C;Superfamily: glucagon

C;Keywords: amidated carboxyl end; duplication; secretagogue; venom

F;39/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 45.5%; Score 60; DB 1; Length 39;
Best Local Similarity 46.2%; Pred. No. 0.02;
Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGL 26
|||||||:|||: | :: :: |
Db 1 HSDGTFTSDL SKQMEEEAVRLFIEWL 26

RESULT 15

GCOPV

glucagon - North American opossum

C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)

C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 20-Mar-1998

C;Accession: JQ0364

R;Yu, J.H.; Eng, J.; Rattan, S.; Yallow, R.S.
Peptides 10, 1195-1197, 1989

A;Title: Opossum insulin, glucagon and pancreatic polypeptide: amino acid sequences.

A;Reference number: JQ0362; MUID:90160042; PMID:2695899

A;Accession: JQ0364

A;Molecule type: protein

A;Residues: 1-29 <YUJ>

C;Superfamily: glucagon

C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas

Query Match 44.7%; Score 59; DB 1; Length 29;
Best Local Similarity 44.4%; Pred. No. 0.02;
Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|| |||||: |: : | | :| |:
Db 1 HSQGTFTSDYSKYLDSRRAQDFVQWLM 27

Search completed: December 4, 2003, 18:08:23

Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2003, 18:07:22 ; Search time 42 Seconds
(without alignments)
102.039 Million cell updates/sec

Title: US-09-897-412-10
Perfect score: 132
Sequence: 1 HSDGTFTSELSRLREGARLQRLLQGLV 27

Scoring table: BLOSUM62
Gapext 0.5 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:
1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

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24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	132	100.0	27	7	AAP60647	Secretin protein s
2	132	100.0	27	17	AAR93024	Human glucagon deg
3	132	100.0	27	21	AAB08187	Amino acid sequenc
4	132	100.0	27	22	AAB70890	Human secretin pep
5	132	100.0	27	22	AAB91261	Secretin peptide S
6	132	100.0	27	23	AAU85988	Modified human sec
7	132	100.0	27	24	ABR40225	Human secretin. H
8	132	100.0	28	10	AAP91869	Human secretin pre
9	132	100.0	31	10	AAP90130	Human secretin. H
10	132	100.0	121	23	AAO21664	Human secreted pro
11	126	95.5	27	22	AAB91259	Secretin peptide S
12	126	95.5	27	24	ABR40227	Canine secretin.
13	123	93.2	27	3	AAP20383	Protected heptacos
14	123	93.2	27	3	AAP20398	Secretin precursor
15	123	93.2	27	4	AAP30021	Synthetic secretin
16	123	93.2	27	4	AAP30014	27-Desamidosecreti
17	123	93.2	27	4	AAP30038	Pig Secretin. Sus
18	123	93.2	27	19	AAW71676	Secretin-derived t
19	123	93.2	27	19	AAW37793	Porcine secretin p
20	123	93.2	27	20	AAY50236	Neutrophil-activat
21	123	93.2	27	22	AAB70901	Porcine secretin p
22	123	93.2	27	22	AAB91262	Secretin peptide S
23	123	93.2	27	22	AAB50844	Pig protein calmod
24	123	93.2	27	23	AAE23659	Heptacosipeptide,
25	123	93.2	27	23	AAE23673	Heptacosipeptide,
26	123	93.2	27	23	ABB08014	Human secretin hep
27	123	93.2	27	23	ABB81203	Secretin heptacosi
28	123	93.2	27	23	ABB06679	Mammalian VIP fami
29	123	93.2	27	23	ABB04453	Secretin derived p
30	123	93.2	27	24	ABR40226	Porcine secretin.
31	123	93.2	27	24	ABP56898	Secretin heptacosi
32	123	93.2	28	4	AAP30063	Recombinantly prod
33	123	93.2	28	4	AAP30062	27-desamidosecreti
34	123	93.2	33	8	AAP70421	Sequence encoded b
35	121	91.7	27	19	AAW37796	Porcine secretin p
36	119	90.2	27	22	AAB91263	Secretin peptide S
37	116	87.9	27	4	AAP30049	Intermediate in se
38	116	87.9	27	24	ABU07569	Human secretin hor
39	116	87.9	30	7	AAP60646	Mammalian secretin
40	115	87.1	27	4	AAP30551	Sequence of 27-Dea
41	108	81.8	26	22	AAB91264	Secretin peptide S
42	103	78.0	27	19	AAW37795	Porcine secretin p
43	92	69.7	27	19	AAW37794	Rabbit secretin pe
44	78	59.1	27	22	AAB91260	Secretin peptide S
45	70	53.0	17	3	AAP20400	Secretin precursor

ALIGNMENTS

RESULT 1

AAP60647

ID AAP60647 standard; peptide; 27 AA.

XX

AC AAP60647;

XX

DT 25-MAR-2003 (updated)

DT 23-JUN-1991 (first entry)

XX

DE Secretin protein sequence.

XX

KW Secretin; hormone.

XX

OS Homo sapiens.

XX

PN WO8605494-A.

XX

PD 25-SEP-1986.

XX

PF 07-MAR-1986; 86WO-SE00099.

XX

PR 11-MAR-1985; 85SE-0001202.

XX

PA (KABI) KABIGEN AB.

PA (CARL/) CARLQUIST M.

PA (SKAN-) SKANDIGEN AB.

XX

PI Carlquist M, Jornvall H, Forssmann W, Thulin L, Johansson C;

PI Mutt V;

XX

DR WPI; 1986-264936/40.

XX

PT Human intestinal hormone secretin isolated from human duodeni -

PT useful as diagnostic to determine pancreatic and gall bladder

PT functions and therapeutically to treat gastro-intestinal

PT disorders.

XX

PS Claim 1; Page 8; 10pp; English.

XX

CC The sequence encodes the human intestinal hormone, secretin,
CC which stimulates secretion of water and bicarbonate from the
CC pancreas. It can be used diagnostically to determine pancreatic
CC and gall bladder functions, or therapeutically to treat gastro-
CC intestinal disorders.

CC (Updated on 25-MAR-2003 to correct PA field.)

XX

SQ Sequence 27 AA;

Query Match 100.0%; Score 132; DB 7; Length 27;

Best Local Similarity 100.0%; Pred. No. 4.6e-12;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSDGTFTSEL SRLREGARLQRLLQGLV 27

||||| ||||| ||||| ||||| ||||| |||||

Db 1 HSDGTFTSEL SRLREGARLQRLLQGLV 27

RESULT 2

AAR93024

ID AAR93024 standard; Protein; 27 AA.

XX

AC AAR93024;

XX

DT 09-AUG-1996 (first entry)

XX

DE Human glucagon degrading enzyme - selectin substrate.

XX

KW Glucagon degrading enzyme; catalyst; cleavage; selectin; human; primer;
KW vasoactive intestinal peptide; VIP; pancreatic carcinoma cell line; PCR;
KW amplification; polymerase chain reaction; probe; expression vector;
KW eukaryote; SV40 promoter; COS-7.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cleavage-site 14..15

FT Modified-site 27

FT /note= "contains C-terminal amide group"

XX

PN JP08023972-A.

XX

PD 30-JAN-1996.

XX

PF 19-JUL-1994; 94JP-0187936.

XX

PR 19-JUL-1994; 94JP-0187936.

XX

PA (SUNR) SUNTORY LTD.

XX

DR WPI; 1996-133414/14.

XX

PT New glucagon decomposing enzyme, and DNA encoding it - for
PT specifically cleaving glucagon and vasoactive intestinal peptide, in
PT the prevention and treatment of diseases caused by excess glucagon
PT and VIP

XX

PS Claim 1; Page 2; 18pp; Japanese.

XX

CC A novel gene encoding a glucagon degrading enzyme (GDE; AAT11575) was
CC isolated from a human pancreatic carcinoma cell line HPC-Yo cDNA
CC library. The enzyme has a mol. wt. 83 kD, a pH optimum of 6.8 and
CC catalyses the cleavage of glucagon, vasoactive intestinal peptide and
CC selectin (AAR93022-4). The gene encoding the enzyme was isolated by
CC screening the library with an anti-GDE peptide antibody, amplifying the
CC inserts with the primers AAT18903-4 and probing the fragments with the
CC probe AAT18905. This screening resulted in the full length clone
CC designated lambda GDE4-2. The coding region of the clone was subsequently
CC PCR amplified by the primers AAT11576-7 and inserted into the eukaryotic
CC expression vector pkDCR under control of the SV40 promoter for
CC production of the protein in COS-7 cells. The protein is useful in
CC preventing and treating diseases characterised by an excess of glucagon
CC or vasoactive intestinal peptide.

XX

SQ Sequence 27 AA;

Query Match 100.0%; Score 132; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.6e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||| | | | | | | | | | | | | | | | | | | | | |
Db 1 HSDGTFTSELSRLREGARLQRLLQGLV 27

RESULT 3
AAB08187
ID AAB08187 standard; Protein; 27 AA.
XX
AC AAB08187;
XX
DT 04-DEC-2000 (first entry)
XX
DE Amino acid sequence of rat secretin polypeptide.
XX
KW Secretin; gastrointestinal hormone; pancreatic fluid; S cell;
KW pancreatic cell growth; pancreatic beta cell; pancreatic islet;
KW insulin production; glucose metabolism; insulin resistance;
KW glucose intolerance; hyperglycemia; hyperinsulinemia; obesity;
KW hyperlipidemia; hyperproteinemia; Type II diabetes mellitus.
XX
OS Rattus sp.
XX
PN WO200047721-A2.
XX
PD 17-AUG-2000.
XX
PF 10-FEB-2000; 2000WO-US03422.
XX
PR 10-FEB-1999; 99US-0119575.
XX
PA (ONTO-) ONTOGENY INC.
XX
PI Kagan D, Pang K;
XX
DR WPI; 2000-515058/46.
DR N-PSDB; AAA63812.
XX
PT Secretin therapeutic is used to modulate the growth state of pancreatic
PT cells to provide treatment for diabetes through modification of glucose
PT metabolism -
XX
PS Claim 8; Page 86; 90pp; English.
XX
CC The present sequence represents a rat secretin polypeptide. Secretin
CC is a gastrointestinal hormone that stimulates the secretion of
CC bicarbonate-rich pancreatic fluid. Secretin is produced by specific
CC endocrine cells (S cells) located in the mucosa of the proximal small
CC intestine. Secretion of secretin is stimulated by the presence of either
CC acidic pH or fatty acids in the duodenum. The specification describes
CC a method for modulating the growth state of pancreatic cells. The method
CC comprises contacting the cells with a secretin therapeutic or prodrug

CC form of secretin. Secretin is used to modulate the growth state of
CC pancreatic cells, in particular to promote the proliferation of
CC pancreatic cells, generate functional pancreatic beta cells from
CC pancreatic islets or cells, promote insulin production in a pancreatic
CC islet or cell, antagonize insulin inhibition of secretin response in
CC secretin-responsive cells, modify glucose metabolism in an animal to
CC treat a disease associated with altered glucose metabolism e.g. insulin
CC resistance, glucose intolerance or non-responsiveness, hyperglycemia,
CC hyperinsulinemia, obesity, hyperlipidemia, hyperproteinemia or Type II
CC diabetes mellitus (NIDD).

XX

SQ Sequence 27 AA;

Query Match 100.0%; Score 132; DB 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.6e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 HSDGTFTSELSRLREGARLQRLLQGLV 27

RESULT 4

AAB70890

ID AAB70890 standard; peptide; 27 AA.

XX

AC AAB70890;

XX

DT 26-JUL-2001 (first entry)

XX

DE Human secretin peptide.

XX

KW Secretin; human; nootropic; autism; treatment; prevention.

XX

OS Homo sapiens.

XX

PN WO200132196-A1.

XX

PD 10-MAY-2001.

XX

PF 03-NOV-2000; 2000WO-EP10847.

XX

PR 05-NOV-1999; 99DE-1053339.

XX

PA (GOLD-) GOLDHAM PHARMA GMBH.

XX

PI Frank A, Jordan K, Hiebl W;

XX

DR WPI; 2001-335783/35.

XX

PT Pharmaceutical composition for selective treatment of autism,
PT containing oligopeptide fragment of secretin, e.g.

PT His-Ser-Asp-Gly-Thr-Phe-Thr-Ser -

XX

PS Disclosure; Page 11; 21pp; German.

XX

CC This invention describes novel pharmaceutical compositions containing at

CC least one secretin peptide fragment having 4-15 (preferably 4-8) amino acids (optionally in acid addition salt form) and which have nootropic activity. The peptide fragments described in the invention (of any origin, e.g. derived from human, porcine, chicken or simian secretin) have a specific beneficial action in the treatment or prevention of autism. They are free of the other activities (e.g. gastrointestinal effects) of secretin itself. This sequence represents the human secretin peptide used to generate the peptide fragments described in the method of the invention.

XX

SQ Sequence 27 AA;

Query Match 100.0%; Score 132; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.6e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 HSDGTFTSELSRLREGARLQRLLQGLV 27

RESULT 5

AAB91261

ID AAB91261 standard; Peptide; 27 AA.

XX

AC AAB91261;

XX

DT 22-JUN-2001 (first entry)

XX

DE Secretin peptide SEQ ID NO:437.

XX

KW Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200069900-A2.

XX

PD 23-NOV-2000.

XX

PF 17-MAY-2000; 2000WO-US13576.

XX

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX

PA (CONJ-) CONJUCHEM INC.

XX

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX

DR WPI; 2001-112059/12.

XX

PT Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity

PT -

xx

PS Disclosure; Page 341; 733pp; English.

xx

CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

xx

SQ Sequence 27 AA;

Query Match 100.0%; Score 132; DB 22; Length 27;
 Best Local Similarity 100.0%; Pred. No. 4.6e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

Pb 1 HSDGTFTSELSRIBREGARLORILOGLY 27

Digitized by srujanika@gmail.com

RESULT 6

AAU85988

ID AAU85988 standard; peptide; 27 AA.

xx

AC AAU85988;

xx

DT 21-MAY-2002 (first entry)

xx

DE Modified human secretin peptide.
XX

XXI

KW increased biological potency; prolonged activity; increased half-life;
KW glucose intolerance; insulin resistance; type II diabetes; bone disease;
KW cancer; inflammatory disorder; obesity; developmental disorder;
KW hyperproliferative skin disease; hormone-dependent disease; homeostasis;
KW intestinal disease; interleukin-8 production; smooth muscle contraction;
KW feeding; blood pressure; pancreatic secretion; mutant; mutein; human;
KW secretin.

xx

OS *Homo sapiens*.

OS Synthetic.

xx

FT Modified-site

FT /note= "H-His"

FT Modified-site 27

FT /note= "C-terminal amide"
XX
PN WO200210195-A2.
XX
PD 07-FEB-2002.
XX
PF 02-AUG-2001; 2001WO-CA01119.
XX
PR 02-AUG-2000; 2000US-222619P.
XX
PA (THER-) THERATECHNOLOGIES INC.
XX
PI Gravel D, Habi A, Abribat T;
XX
DR WPI; 2002-206179/26.
XX
PT Novel modified biological peptide with increased biological potency,
PT prolonged activity, increased half-life, for treating glucose
PT intolerance associated or not with insulin resistance pathologies, type
PT II diabetes -
XX
PS Claim 5; Page 62; 77pp; English.
XX
CC The present invention relates to modified biological peptides with
CC increased biological potency, prolonged activity and/or increased
CC half-life. The peptides of the invention are useful in the treatment
CC of glucose intolerance which may be associated with insulin resistance
CC pathologies, and in the treatment of type II diabetes. They are also
CC useful for treating bone diseases, cancer, diseases related to
CC inflammatory responses, obesity, autism, pervasive developmental
CC disorders, hyperproliferative skin diseases, hormone-dependent diseases,
CC They can be used for regulating blood glucose, enhancing mucosal
CC regeneration in patients with intestinal diseases, inhibition of
CC interleukin-8 production, stimulation of acid release, homeostasis,
CC regulation of exocrine and endocrine secretions, smooth muscle
CC contraction, feeding, blood pressure, body temperature and cell growth,
CC regulation of food intake and energy balance, and stimulation of
CC pancreatic secretion or cell growth. AAU85971-AAU86019 represent the
CC modified biological peptides of the invention.
XX
SQ Sequence 27 AA;

Query Match 100.0%; Score 132; DB 23; Length 27;
 Best Local Similarity 100.0%; Pred. No. 4.6e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
ABR40225
ID ABR40225 standard; peptide; 27 AA.
XX
AC ABR40225;
XX

DT 12-JUN-2003 (first entry)
XX
DE Human secretin.
XX
KW Human; asthma; anion efflux; secretin receptor; antiasthmatic; secretin.
XX
OS Homo sapiens.
XX
PN WO2003011327-A2.
XX
PD 13-FEB-2003.
XX
PF 26-JUL-2002; 2002WO-GB03433.
XX
PR 27-JUL-2001; 2001GB-0018383.
XX
PA (PHAR-) PHARMAGENE LAB LTD.
XX
PI Davis RJ, Clark K;
XX
DR WPI; 2003-248115/24.
XX
PT Treating asthma in a patient suffering from asthma, by administering to
PT the patient an agent e.g., secretin which triggers anion efflux in
PT respiratory tissue by the activation of a secretin receptor -
XX
PS Disclosure; Fig 1; 40pp; English.
XX
CC The invention relates to a novel method for treating asthma in a patient
CC suffering from asthma, involving administering to the patient an
CC effective amount of an agent which triggers anion efflux in respiratory
CC tissue by the activation of a secretin receptor. The method of the
CC invention has antiasthmatic activity. The method is useful for treating
CC asthma in a patient. The present sequence is used in the exemplification
CC of the invention.
XX
SQ Sequence 27 AA;

Query Match 100.0%; Score 132; DB 24; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.6e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 HSDGTFTSELSRLREGARLQRLLQGLV 27

RESULT 8
AAP91869
ID AAP91869 standard; peptide; 28 AA.
XX
AC AAP91869;
XX
DT 25-MAR-2003 (updated)
DT 02-FEB-1990 (first entry)
XX
DE Human secretin precursor.

XX Human secretin precursor; anti-ulcer.
XX
OS Homo sapiens.
XX
PN JP01215296-A.
XX
PD 29-AUG-1989.
XX
PF 23-FEB-1988; 88JP-0041615.
XX
PR 23-FEB-1988; 88JP-0041615.
XX
PA (WAKT) WAKUNAGA SEIYAKU KK.
XX
DR WPI; 1989-290775/40.
DR N-PSDB; AAN91221.
XX
PT Human secretin precursor, for antiulcer drug - is prep'd. by prepn. of
PT human secretin precursor-coding gene, prepn. of recombinant vector, etc.
XX
PS Claim 1; page 649; 5pp; japanese.
XX
CC The peptide has the drug effect of secretin, but has stronger biological
CC activity than natural secretin. It is used as an anti-ulcer drug. It is
CC recovered from Escherichia sp. transformed with a vector contg. the
CC peptide gene by acid extn., removal of impurities by alkali addn., and
CC purificn. by reverse phase chromatography. X= GKR; GK; GR; GRK; or
CC is absent.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 132; DB 10; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
AAP90130
ID AAP90130 standard; protein; 31 AA.
XX
AC AAP90130;
XX
DT 25-MAR-2003 (updated)
DT 01-NOV-1989 (first entry)
XX
DE Human secretin.
XX
KW Human secretin; fusion protein; recombinant vector.
XX
OS Homo sapiens (Human).
XX

PN JP01144981-A.
XX
PD 07-JUN-1989.
XX
PF 02-DEC-1987; 87JP-0304937.
XX
PR 02-DEC-1987; 87JP-0304937.
XX
PA (WAKT) WAKUNAGA SEIYAKU KK.
XX
DR WPI; 1989-209284/29.
DR N-PSDB; AAN90270.
XX
PT Recombinant vector contg. fusion protein
PT - consisting of human growth hormone or deriv. ligated
PT to foreign protein, for stability and high yield.
XX
PS Disclosure; fig 3; 19pp; Japanese.
XX
CC Human secretin (see AAN90270). The invention
CC consists of a vector contg. a fusion protein which is formed
CC by ligating, downstream of a promoter, human growth hormone or a
CC deriv. (see AAN90269) and a foreign protein. Stability of the vector
CC in the host is greatly increased so the protein yield is higher.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 132; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.3e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2 HSDGTFTSELSRLREGARLQRLLQGLV 28

RESULT 10
AAO21664
ID AAO21664 standard; Protein; 121 AA.
XX
AC AAO21664;
XX
DT 05-SEP-2002 (first entry)
XX
DE Human secreted protein SEQ ID No 6.
XX
KW Antiarteriosclerotic; cytostatic; HIV; antiallergic; antianaemic;
KW antiasthmatic; cardiant; vasotropic; neuroprotective; nootropic; SECP;
KW anticonvulsant; antiparkinsonian; cerebroprotective; antiinflammatory;
KW immunosuppressive; human secreted protein; cell proliferative disorder;
KW arteriosclerosis; cancer; autoimmune; inflammatory disorder; AIDS;
KW allergy; anaemia; asthma; cardiovascular disease; developmental disorder;
KW ischaemic heart disease; congestive heart failure; neurological disorder;
KW renal tubular acidosis; hypothyroidism; Alzheimer's disease; dementia;
KW Parkinson's disease; epilepsy; stroke; knockin humanised animal;
KW transgenic animal; gene therapy.

XX
OS Homo sapiens.
XX
PN WO200238602-A2.
XX
PD 16-MAY-2002.
XX
PF 08-NOV-2001; 2001WO-US47420.
XX
PR 08-NOV-2000; 2000US-247505P.
PR 09-NOV-2000; 2000US-248642P.
PR 16-NOV-2000; 2000US-249824P.
PR 21-NOV-2000; 2000US-252824P.
PR 08-DEC-2000; 2000US-254305P.
PR 18-DEC-2000; 2000US-256448P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Yue H, Yao MG, Gandhi AR, Baughn MR, Swarnakar A, Walia NK;
PI Sanjanwala M, Thornton M, Elliott VS, Lu Y, Gietzen KJ, Burford N;
PI Ding L, Hafalia AJA, Tang YT, Bandman O, Warren BA, Honchell CD;
PI Lu DAM, Thangavelu K, Lee S, Xu Y, Yang J, Lal PG, Tran B;
PI Ison CH, Duggan BM, Sapperstein SK;
XX
DR WPI; 2002-519296/55.
DR N-PSDB; AAL39625.
XX
PT Human secreted proteins and polynucleotides for diagnosing, treating or
PT preventing disorders of cell proliferative, cardiovascular,
PT developmental, neurological and autoimmune/inflammatory disorders -
XX
PS Claim 1; Page 156; 229pp; English.
XX
CC The invention relates to an isolated human secreted protein (SECP)
CC polypeptide from 63 fully defined protein sequences given in the
CC specification. The polypeptide is useful for the diagnosing/treating of a
CC disease with decreased/overexpression of SECP. Examples of disorders
CC associated with abnormal expression of SECP include a cell proliferative
CC disorder e.g. arteriosclerosis, cancers; autoimmune/inflammatory
CC disorder, AIDS, allergies, anaemia, asthma; cardiovascular disease e.g.
CC congestive heart failure, ischaemic heart disease; developmental disorder
CC e.g. renal tubular acidosis, hypothyroidism; neurological disorder e.g.
CC Alzheimer's disease, dementia, Parkinson's disease, epilepsy or stroke.
CC The SECP polynucleotide and polypeptide are further useful for analysing
CC the proteome of a tissue or a cell type. The polynucleotide is useful for
CC creating knockin humanised animals (pigs) or transgenic animals (mice or
CC rats) to model human disease, and for somatic or germline gene therapy,
CC and further for generating hybridisation probes useful in mapping the
CC naturally occurring genomic sequence. This sequence represents a human
CC secreted protein of the invention.
XX
SQ Sequence 121 AA;

Query Match 100.0%; Score 132; DB 23; Length 121;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
| | | | | | | | | | | | | | | | | |
Db 28 HSDGTFTSELSRLREGARLQRLLQGLV 54

RESULT 11

AAB91259

ID AAB91259 standard; Peptide; 27 AA.

XX

AC AAB91259;

XX

DT 22-JUN-2001 (first entry)

XX

DE Secretin peptide SEQ ID NO:435.

XX

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200069900-A2.

XX

PD 23-NOV-2000.

XX

PF 17-MAY-2000; 2000WO-US13576.

XX

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX

PA (CONJ-) CONJUCHEM INC.

XX

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX

DR WPI; 2001-112059/12.

XX

PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity

PT -

XX

PS Disclosure; Page 340; 733pp; English.

XX

CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half

CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX

SQ Sequence 27 AA;

Query Match 95.5%; Score 126; DB 22; Length 27;
Best Local Similarity 96.3%; Pred. No. 3.4e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 HSDGTFTSELSRLRESARLQRLLQGLV 27

RESULT 12

ABR40227

ID ABR40227 standard; peptide; 27 AA.

XX

AC ABR40227;

XX

DT 12-JUN-2003 (first entry)

XX

DE Canine secretin.

XX

KW Dog; asthma; anion efflux; secretin receptor; antiasthmatic; secretin.

XX

OS Canis sp.

XX

PN WO2003011327-A2.

XX

PD 13-FEB-2003.

XX

PF 26-JUL-2002; 2002WO-GB03433.

XX

PR 27-JUL-2001; 2001GB-0018383.

XX

PA (PHAR-) PHARMAGENE LAB LTD.

XX

PI Davis RJ, Clark K;

XX

DR WPI; 2003-248115/24.

XX

PT Treating asthma in a patient suffering from asthma, by administering to
PT the patient an agent e.g., secretin which triggers anion efflux in
PT respiratory tissue by the activation of a secretin receptor -

XX

PS Disclosure; Fig 1; 40pp; English.

XX

CC The invention relates to a novel method for treating asthma in a patient
CC suffering from asthma, involving administering to the patient an
CC effective amount of an agent which triggers anion efflux in respiratory
CC tissue by the activation of a secretin receptor. The method of the
CC invention has antiasthmatic activity. The method is useful for treating
CC asthma in a patient. The present sequence is used in the exemplification
CC of the invention.

XX
SQ Sequence 27 AA;
Query Match 95.5%; Score 126; DB 24; Length 27;
Best Local Similarity 96.3%; Pred. No. 3.4e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||| ||| ||| ||| ||| |||
Db 1 HSDGTFTSELSRLRESARLQRLLQGLV 27

RESULT 13
AAP20383
ID AAP20383 standard; peptide; 27 AA.

XX
AC AAP20383;

XX
DT 25-MAR-2003 (updated)
DT 30-NOV-1992 (first entry)

XX
DE Protected heptacosapeptide.

XX
KW Secretin; pancreatic juices; gastric juices.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "p-methoxybenzyloxycarbonyl-protected"
FT Modified-site 12
FT /note= "NG-mesitylene sulphonylarginine"
FT Modified-site 14
FT /note= "NG-mesitylene sulphonylarginine"
FT Modified-site 18
FT /note= "NG-mesitylene sulphonylarginine"
FT Modified-site 21
FT /note= "NG-mesitylene sulphonylarginine"

XX
PN JP56158747-A.

XX
PD 07-DEC-1981.

XX
PF 19-OCT-1979; 79JP-0086417.

XX
PR 15-NOV-1979; 79JP-0148350.

XX
PA (NNSH) NIPPON SHINYAKU CO LTD.

XX
DR WPI; 1982-04870E/03 (04870E).

XX
PT Para:methoxy:benzyloxy:carbonyl protected heptacosa:peptide - is
PT intermediate for secretin, which e.g. stimulates pancreatic
PT juices

XX
PS Claim 1; Page 1; 5pp; Japanese.

XX

CC The sequence given is a heptacosapeptide which can be used as a
CC precursor for secretin production. Secretin is a digestive tract
CC enzyme which has physiological actions such as pancreatic juice
secretion-stimulating action and gastric juice secretion-inhibiting
CC action. The heptacosapeptide can be converted to secretin by
treating it with CF3SO3H. This yields large amounts of high purity
CC secretin in a short time.
CC (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 27 AA;

Query Match 93.2%; Score 123; DB 3; Length 27;
Best Local Similarity 92.6%; Pred. No. 9.2e-11;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|||:|||||:|||||:
Db 1 HSDGTFTSELSRLRDSARLQRLLQGLV 27

RESULT 14
AAP20398
ID AAP20398 standard; peptide; 27 AA.
XX
AC AAP20398;
XX
DT 25-MAR-2003 (updated)
DT 30-NOV-1992 (first entry)
XX
DE Secretin precursor peptide.
XX
KW Strong acid; digestive canal hormone; pancreas; gastrin; pepsin;
KW insulin.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Boc protected"
FT Modified-site 2
FT /note= "But protected"
FT Modified-site 3
FT /note= "OBut protected"
FT Modified-site 5
FT /note= "But protected"
FT Modified-site 7
FT /note= "But protected"
FT Modified-site 8
FT /note= "But protected"
FT Modified-site 9
FT /note= "OBut protected"
FT Modified-site 11
FT /note= "But protected"
FT Modified-site 12
FT /note= "PhSO2 ring subst. by 1, 2 or 3 alkyl or
alkoxy gps."

FT Modified-site 14
FT /note= "PhSO₂ ring subst. by 1, 2 or 3 alkyl or
FT alkoxy gps."
FT Modified-site 15
FT /note= "OBut protected"
FT Modified-site 16
FT /note= "But protected"
FT Modified-site 18
FT /note= "PhSO₂ ring subst. by 1, 2 or 3 alkyl or
FT alkoxy gps."
FT Modified-site 21
FT /note= "PhSO₂ ring subst. by 1, 2 or 3 alkyl or
FT alkoxy gps."
XX
PN EP47997-A.
XX
PD 24-MAR-1982.
XX
PF 11-SEP-1981; 81EP-0107186.
XX
PR 11-SEP-1980; 80JP-0125262.
XX
PA (EISA) EISAI CO LTD.
XX
PI Uchiyama M, Sato T, Yoshino H, Tsuchiya Y, Konishi M;
PI Tsujii M, Hisatake Y, Koiwa A;
XX
DR WPI; 1982-24409E/13 (24409E).
XX
PT Heptacosa:peptide(s) - useful for high yield conversion to high
PT purity secretin on strong acid treatment
XX
PS Claim 1; Page 43; 47pp; English.
XX
CC The sequence in AAP20398 is a precursor for the production of
CC secretin. The peptide sequences given in AAP20399-402 are peptides
CC which are useful in the production of this precursor. The precursor is
CC treated with strong acid in the preparation of secretin. Secretin is
CC one of the digestive canal hormones and is useful in promotion of
CC pancreatic external secretin, controlling gastrin-stimulating secretin
CC of the stomach acid, releasing insulin, stimulating secretin of pepsin
CC and decomposing fat. It is used as a pancreatic-function examining
CC agent and a medicine for curing duodenal ulcers etc.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 27 AA;

Query Match 93.2%; Score 123; DB 3; Length 27;
Best Local Similarity 92.6%; Pred. No. 9.2e-11;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
||| ||| ||| ||| : ||| ||| ||| |||
Db 1 HSDGTFTSELSRLRDSARLQRLLQGLV 27

RESULT 15

AAP30021
ID AAP30021 standard; peptide; 27 AA.
XX
AC AAP30021;
XX
DT 25-MAR-2003 (updated)
DT 03-SEP-1992 (first entry)
XX
DE Synthetic secretin.
XX
KW Pharmaceutically; deprotection; digestive; hormone; pancreatism;
KW duodenal ulcer.
XX
OS Synthetic.
XX
PN JP58144355-A.
XX
PD 27-AUG-1983.
XX
PF 22-FEB-1982; 82JP-0026088.
XX
PR 31-MAR-1981; 81JP-0048887.
XX
PA (EISA) EISAI CO LTD.
XX
DR WPI; 1983-779933/40.
XX
PT Pharmaceutically active secretin - prep'd. by removing protective
PT gp. from heptacosa:peptide
XX
PS Claim 3; Page 2; 13pp; Japanese.
XX
CC Secretin, which has hitherto been produced by extraction from
CC porcine duodenum, may be produced by standard solid phase synthesis.
CC Secretin is a digestive tract hormone with many useful
CC pharmaceutical actions such as pancreatic secretion promotion,
CC gastrin stimulation, gastric acid secretion inhibition, insulin
CC release, stimulation of pepsin secretion and lipolytic action. It
CC is useful as a reagent for test on pancreatism and as a remedy for
CC duodenal ulcers.
CC (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 27 AA;

Query Match 93.2%; Score 123; DB 4; Length 27;
Best Local Similarity 92.6%; Pred. No. 9.2e-11;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSDGTFTSELSRLREGARLQRLLQGLV 27
|||:|||||:|||||
Db 1 HSDGTFTSELSRLRDSARLQRLLQGLV 27

Search completed: December 4, 2003, 18:09:19
Job time : 43 secs